

STIC-Biotech/ChemLib

105381

From: Bunner, Bridget
Sent: Monday, October 06, 2003 9:42 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 10/070,240:

1. the amino acid sequence of SEQ ID NO: 1

Thanks!

Bridget Bunner

Art Unit 1647
CM1-10D12
(703) 305-7148
mailbox 10B19

OCT 6 2003
STIC

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 10/7/03
Date Completed: 10/8/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1 _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 02 _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 09:52:17 ; Search time 67 Seconds
(without alignments)
928.025 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTWGPMDDNATNTSFL.....LDLKTIGMPATEEVDICRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PublishedApplications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 2055 | 100.0 | 393 | 12 | US-10-088-726-4 |
| 3 | 2055 | 100.0 | 393 | 15 | US-10-067-649-2 |
| 4 | 2035 | 99.0 | 389 | 9 | US-09-750-373-27 |
| 5 | 2035 | 99.0 | 389 | 10 | US-09-925-922-2 |
| 6 | 2035 | 99.0 | 389 | 15 | US-10-925-922-4 |
| 7 | 2030 | 98.8 | 389 | 12 | US-10-345-680-35 |
| 8 | 1924 | 93.6 | 382 | 15 | US-10-132-812-6 |
| 9 | 1766 | 85.9 | 384 | 12 | US-10-321-807-2 |
| 10 | 1766 | 85.9 | 384 | 15 | US-10-132-812-4 |
| 11 | 1764 | 85.8 | 393 | 15 | US-10-067-649-4 |
| 12 | 1762 | 85.7 | 384 | 9 | US-09-764-556-2 |
| 13 | 1762 | 85.7 | 384 | 15 | US-10-132-812-2 |
| 14 | 1755.5 | 85.4 | 385 | 15 | US-10-220-289-5 |
| 15 | 1703 | 82.9 | 355 | 15 | US-10-067-649-3 |

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|----|-------|------|-----|----|---------------------|-------------------|
| 16 | 1109 | 54.0 | 231 | 15 | US-10-220-289-4 | Sequence 4, Appli |
| 17 | 1042 | 50.7 | 207 | 11 | US-09-782-974C-34 | Sequence 34, Appl |
| 18 | 839 | 40.8 | 254 | 12 | US-10-017-161-1548 | Sequence 1548, Ap |
| 19 | 799 | 38.9 | 217 | 9 | US-09-750-373-19 | Sequence 19, Appl |
| 20 | 657 | 32.0 | 154 | 15 | US-10-220-289-2 | Sequence 2, Appl1 |
| 21 | 589 | 28.7 | 123 | 9 | US-09-864-761-36840 | Sequence 36840, A |
| 22 | 589 | 28.7 | 123 | 9 | US-09-864-761-48506 | Sequence 48506, A |
| 23 | 431 | 21.0 | 86 | 10 | US-09-925-922-4 | Sequence 4, Appl1 |
| 24 | 416.5 | 20.3 | 385 | 15 | US-10-067-649-6 | Sequence 6, Appl1 |
| 25 | 407 | 19.8 | 464 | 12 | US-10-283-423-14 | Sequence 14, Appl |
| 26 | 407 | 19.8 | 464 | 12 | US-10-213-821-14 | Sequence 14, Appl |
| 27 | 407 | 19.8 | 518 | 12 | US-10-383-423-16 | Sequence 16, Appl |
| 28 | 407 | 19.8 | 518 | 12 | US-10-213-821-16 | Sequence 16, Appl |
| 29 | 401.5 | 19.5 | 381 | 12 | US-10-188-619-4 | Sequence 4, Appl1 |
| 30 | 401.5 | 19.5 | 381 | 15 | US-10-067-649-5 | Sequence 5, Appl1 |
| 31 | 395.5 | 19.2 | 381 | 12 | US-10-188-619-6 | Sequence 6, Appl1 |
| 32 | 390.5 | 19.0 | 385 | 11 | US-09-992-331-18 | Sequence 18, Appl |
| 33 | 390.5 | 19.0 | 385 | 16 | US-10-262-313-18 | Sequence 18, Appl |
| 34 | 387.5 | 18.9 | 381 | 10 | US-09-962-646-16 | Sequence 16, Appl |
| 35 | 387.5 | 18.9 | 381 | 10 | US-09-992-973-5 | Sequence 5, Appl1 |
| 36 | 387.5 | 18.9 | 381 | 10 | US-09-992-973-20 | Sequence 20, Appl |
| 37 | 387.5 | 18.9 | 381 | 12 | US-10-188-619-2 | Sequence 2, Appl1 |
| 38 | 387.5 | 18.9 | 381 | 15 | US-10-225-567A-201 | Sequence 201, App |
| 39 | 382 | 18.6 | 522 | 12 | US-10-283-423-12 | Sequence 12, Appl |
| 40 | 382 | 18.6 | 522 | 12 | US-10-213-821-12 | Sequence 12, Appl |
| 41 | 380.5 | 18.5 | 519 | 12 | US-10-283-423-10 | Sequence 10, Appl |
| 42 | 380.5 | 18.5 | 519 | 12 | US-10-213-821-10 | Sequence 10, Appl |
| 43 | 370 | 18.0 | 370 | 12 | US-10-278-087A-26 | Sequence 26, Appl |
| 44 | 370 | 18.0 | 370 | 14 | US-10-044-592-12 | Sequence 12, Appl |
| 45 | 370 | 18.0 | 370 | 14 | US-10-044-592-74 | Sequence 74, Appl |

ALIGNMENTS

RESULT 1
US-09-750-373-26
; Sequence 26, Application US/09750373
; Patent No. US20020062013A1
; GENERAL INFORMATION:
; APPLICANT: Lind Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Hiebsch, Ronald
; APPLICANT: Ruff, Valerie
; APPLICANT: Lindberg, Eleni
; APPLICANT: Parodi, Luis A.
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20020062013A1e1 G Protein Coupled Receptors
; FILE REFERENCE: PHRM-0300
; CURRENT APPLICATION NUMBER: US/09/750,373
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/219,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/173,339
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/224,321
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,534
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/239,062
; PRIOR FILING DATE: 2000-10-09
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-750-373-26

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Best Local Similarity 100.0%; Pred. No. 1.7e-188;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AKIVIGMALVGMVCGIGNFIFTAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCOTAT 180
DB 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCOTAT 180
QY 181 GLIALVMTVSIILAIPSAYFTTETVLVIVKSOEKIFCGQIWPVDQQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSIILAIPSAYFTTETVLVIVKSOEKIFCGQIWPVDQQLYKSYFLFIFGIE 240
QY 241 FVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTAYVLCWAPF 300
DB 241 FVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTAYVLCWAPF 300
QY 301 YGFTIVRDFPFTVFEKHYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
DB 301 YGFTIVRDFPFTVFEKHYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
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DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393

RESULT 2
US-10-088-726-4
; Sequence 4, Application US/10088726
; Publication No. US2003015758A1
; GENERAL INFORMATION:
; APPLICANT: Matsumoto et al.
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AND
; FILE REFERENCE: 62514
; CURRENT APPLICATION NUMBER: US/10/088, 726
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/JP00/09408
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 1999-375152
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: JP 2000-101339
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-088-726-4

Query Match 100.0%; Score 2055; DB 12; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.7e-188;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 YGFTIVRDFPFTVFEKHYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
DB 301 YGFTIVRDFPFTVFEKHYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393

RESULT 3
US-10-067-649-2
; Sequence 2, Application US/10067649
; Publication No. US20030100057A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY14, RELATED :
; FILE REFERENCE: D0118 NP
; CURRENT APPLICATION NUMBER: US/10/067, 649
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/266, 525
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 60/329, 897
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 2
; LENGTH: 393
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-649-2

Query Match 100.0%; Score 2055; DB 15; Length 393;
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Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-750-373-27
; Sequence 27, Application US/09750373
; Patent No. US20020062013A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Hiesch, Ronald
; APPLICANT: Ruff, Valerie
; APPLICANT: Lindberg, Eleni
; APPLICANT: Parodi, Luis A.
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No US20020062013A1 G Protein Coupled Receptors
; FILE REFERENCE: PHRM-0300
; CURRENT APPLICATION NUMBER: US/09/750,373
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/219,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/173,339
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/224,321
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,534
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/239,062
; PRIOR FILING DATE: 2000-10-09
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-750-373-27

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Best Local Similarity 100.0%; Pred. No. 1.4e-186;

Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 65 | IGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV | 124 |
| DB | 61 | IGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV | 120 |
| QY | 125 | VRQLSWEHGHVLTCSVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA | 184 |
| DB | 121 | VRQLSWEHGHVLTCSVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA | 180 |
| QY | 185 | LWTVSILIAIPSAFYTTETVLVIVKSEKIFCGQIWPVQDQLYKSYFLFIFGIEFVGP | 244 |
| DB | 181 | LWTVSILIAIPSAFYTTETVLVIVKSEKIFCGQIWPVQDQLYKSYFLFIFGIEFVGP | 240 |
| QY | 245 | VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRRTVLVLMCILTAIVLCHWAPFYGT | 304 |
| DB | 241 | VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRRTVLVLMCILTAIVLCHWAPFYGT | 300 |
| QY | 305 | IVRDFPFTVFKKHYLTAFIVIECIAMNSMINTLCFVTVKNDTVKFKIMLLHWKAS | 364 |
| DB | 301 | IVRDFPFTVFKKHYLTAFIVIECIAMNSMINTLCFVTVKNDTVKFKIMLLHWKAS | 360 |

RESULT 5

US-09-925-922-2
; Sequence 2, Application US/09925922
; Patent No. US20020165380A1
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA Encoding A Mammalian Receptor (fb4la) And Uses
; FILE REFERENCE: 55182.app
; CURRENT APPLICATION NUMBER: US/09/925,922
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/210,279
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-922-2

Query Match 99.0%; Score 2035; DB 10; Length 389;

Best Local Similarity 100.0%; Pred. No. 1.4e-186;

Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| DB | 1 | MGFMDDNATNTSTFSLVNLPHGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFAAKIV | 60 |
| QY | 65 | IGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV | 124 |
| DB | 61 | IGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV | 120 |
| QY | 125 | VRQLSWEHGHVLTCSVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA | 184 |
| DB | 121 | VRQLSWEHGHVLTCSVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA | 180 |
| QY | 185 | LWTVSILIAIPSAFYTTETVLVIVKSEKIFCGQIWPVQDQLYKSYFLFIFGIEFVGP | 244 |
| DB | 181 | LWTVSILIAIPSAFYTTETVLVIVKSEKIFCGQIWPVQDQLYKSYFLFIFGIEFVGP | 240 |
| QY | 245 | VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRRTVLVLMCILTAIVLCHWAPFYGT | 304 |
| DB | 241 | VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRRTVLVLMCILTAIVLCHWAPFYGT | 300 |
| QY | 305 | IVRDFPFTVFKKHYLTAFIVIECIAMNSMINTLCFVTVKNDTVKFKIMLLHWKAS | 364 |
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| QY | 365 | YNGKSSADLDLKTIGMPATEEVDICRLK | 393 |
| DB | 361 | YNGKSSADLDLKTIGMPATEEVDICRLK | 389 |

RESULT 6

US-10-225-567A-678

; Sequence 678, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: Lifespan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenn C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEP

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 678

; LENGTH: 389

; TYPE: PRT


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; ORGANISM: Homo sapiens
US-10-225-567A-678

Query Match          99.0%; Score 2035; DB 15; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.4e-186;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYDMDPLDEDEDVTSRTFFAAKIV 60
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QY 65 IGMALVGMVLCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFVAIVCCPFEMDYV 124
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Db 61 IGMALVGMVLCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFVAIVCCPFEMDYV 120
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QY 125 VROLSEHGVLCTSVNLTSTVSLVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA 184
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Db 181 LWMTVSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 240
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Db 241 VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGT 300
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QY 305 IYRDFEPTVFKKHYLTAFYIVECIAMNSMINTLCFTVTKNDTVKYFKKIMLLHWKAS 364
   |||||
Db 301 IYRDFEPTVFKKHYLTAFYIVECIAMNSMINTLCFTVTKNDTVKYFKKIMLLHWKAS 360
   |||||

QY 365 YNGKSSADLDLKTIGMPATEEVDICRLK 393
   |||||
Db 361 YNGKSSADLDLKTIGMPATEEVDICRLK 389
   |||||

RESULT 7
US-10-345-680-35
; Sequence 35, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Imaculada
; APPLICANT: Venkateswari, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PLRNM-OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 389

; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-345-680-35

Query Match          98.8%; Score 2030; DB 12; Length 389;
Best Local Similarity 99.7%; Pred. No. 4.2e-186;
Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 MGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYDMDPLDEDEDVTSRTFFAAKIV 64
   |||||
Db 1 MGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYDMDPLDEDEDVTSRTFFAAKIV 60
   |||||

QY 65 IGMALVGMVLCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFVAIVCCPFEMDYV 124
   |||||
Db 61 IGMALVGMVLCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFVAIVCCPFEMDYV 120
   |||||

QY 125 VROLSEHGVLCTSVNLTSTVSLVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA 184
   |||||
Db 121 VROLSEHGVLCTSVNLTSTVSLVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA 180
   |||||

QY 185 LWMTVSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 244
   |||||
Db 181 LWMTVSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 240
   |||||

QY 245 VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGT 304
   |||||
Db 241 VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGT 300
   |||||

QY 305 IYRDFEPTVFKKHYLTAFYIVECIAMNSMINTLCFTVTKNDTVKYFKKIMLLHWKAS 364
   |||||
Db 301 IYRDFEPTVFKKHYLTAFYIVECIAMNSMINTLCFTVTKNDTVKYFKKIMLLHWKAS 360
   |||||

QY 365 YNGKSSADLDLKTIGMPATEEVDICRLK 393
   |||||
Db 361 YNGKSSADLDLKTIGMPATEEVDICRLK 389
   |||||

RESULT 8
US-10-132-812-6
; Sequence 6, Application US/10132812
; Publication No. US20030059856A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Sarau, Henry M.
; APPLICANT: Slemmon, J. Randall
; APPLICANT: McNulty, Dean E.
; APPLICANT: Vawter, Lisa
; APPLICANT: Foley, James J.
; TITLE OF INVENTION: Methods Of Screening For Agonists And
; TITLE OF INVENTION: Agonists Of The Interaction Between The AXOR8 And AXOR52
; TITLE OF INVENTION: Receptors And Ligands Thereof
; FILE REFERENCE: P51256
; CURRENT APPLICATION NUMBER: US/10/132,812
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,234
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-812-6

Query Match          93.6%; Score 1924; DB 15; Length 382;
Best Local Similarity 100.0%; Pred. No. 5.8e-176;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTWGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYDMDPLDEDEDVTSRTFFA 60
   |||||
Db 1 MFTWGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYDMDPLDEDEDVTSRTFFA 60
   |||||

QY 61 AKIVIGMALVGMVLCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFVAIVCCPFEM 120
   |||||
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Db 61 AKIVIGMALVGHMLVCGIGNFIFIAALVRYKKLRNLTLNLIANLAISDFLVAIVCCPFEMDYYVVRQLSWE 120
Qy 121 DYVVVQLSWEHGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCOTAT 180
Db 121 DYVVVQLSWEHGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCOTAT 180
Qy 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQOLYKSYFLFIFGIE 240
Db 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQOLYKSYFLFIFGIE 240
Qy 241 FVGPVVTMTLCYARISRELWFAVPGFQEQIRKRLCRKRTVLVLMCILTAIVLCWAPF 300
Db 241 FVGPVVTMTLCYARISRELWFAVPGFQEQIRKRLCRKRTVLVLMCILTAIVLCWAPF 300
Qy 301 YGFTIVRDFFPTVFKKHYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLH 360
Db 301 YGFTIVRDFFPTVFKKHYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLH 360
Qy 361 WKASYNG 367
Db 361 WKASYNG 367

RESULT 9
US-10-321-807-2
; Sequence 2, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruqong
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2000-11-16
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-2

Query Match 85.9%; Score 1766; DB 12; Length 384;
Best Local Similarity 87.4%; Pred. No. 7.8e-161;
Matches 334; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Qy 12 ATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDEDEDVTSRTFFAAKIVIGMALVG 71
Db 3 AQNGNTSPTPNFPNPPQDHASSLSFNFSYGDYDLPDDEDEDMTKTRTFFAKIVIGIALAG 62

Qy 72 IMLVCGIGNFIFIAALVRYKKLRNLTLNLIANLAISDFLVAIVCCPFEMDYYVVRQLSWE 131
Db 63 IMLVCGIGNFIFIAALVRYKKLRNLTLNLIANLAISDFLVAIVCCPFEMDYYVVRQLSWE 122

Qy 132 HGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCOTATGLIALVWTVSI 191
Db 123 HGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCOTATGLIALVWTVSI 182

Qy 192 LIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQOLYKSYFLFIFGIEFVGPVVTMTLC 251
Db 183 LIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQOLYKSYFLFIFGIEFVGPVVTMTLC 242

Qy 252 YARISRELWFAVPGFQEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGFTIVRDFFP 311
Db 243 YARISRELWFAVPGFQEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGFTIVRDFFP 302

Qy 312 TVFVKEKHLYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLHWKASYNGSKSS 371
Db 303 TVFVKEKHLYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLHWKASYNGSKSS 362

Qy 372 ADLKLKTIGMPATEEVDICRLK 393
Db 363 ADLKLRTNSVPTTEEVDICRLK 384

RESULT 10
US-10-132-812-4
; Sequence 4, Application US/10132812
; Publication No. US20030059856A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Sarau, Henry M.
; APPLICANT: Slemon, J. Randall
; APPLICANT: McNulty, Dean E.
; APPLICANT: Vawter, Lisa
; APPLICANT: Foley, James J.
; TITLE OF INVENTION: Methods Of Screening For Agonists And
; TITLE OF INVENTION: Agonists Of The Interaction Between The AXOR8 And AXOR52
; TITLE OF INVENTION: Receptors And Ligands Thereof
; FILE REFERENCE: P51256
; CURRENT APPLICATION NUMBER: US/10/132,812
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,234
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-812-4

Query Match 85.9%; Score 1766; DB 15; Length 384;
Best Local Similarity 87.4%; Pred. No. 7.8e-161;
Matches 334; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Qy 12 ATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDEDEDVTSRTFFAAKIVIGMALVG 71
Db 3 AQNGNTSPTPNFPNPPQDHASSLSFNFSYGDYDLPDDEDEDMTKTRTFFAKIVIGIALAG 62

Qy 72 IMLVCGIGNFIFIAALVRYKKLRNLTLNLIANLAISDFLVAIVCCPFEMDYYVVRQLSWE 131
Db 63 IMLVCGIGNFIFIAALVRYKKLRNLTLNLIANLAISDFLVAIVCCPFEMDYYVVRQLSWE 122

Qy 132 HGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCOTATGLIALVWTVSI 191
Db 123 HGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCOTATGLIALVWTVSI 182

Qy 192 LIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQOLYKSYFLFIFGIEFVGPVVTMTLC 251
Db 183 LIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQOLYKSYFLFIFGIEFVGPVVTMTLC 242
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QY 252 YARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGTIVRDFEP 311
DB 243 YARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGTIVRDFEP 302
QY 312 TVFVKEKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVKYFKKIMLHMKASYNGKSS 371
DB 303 TVFVKEKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVKYFKKIMLHMKASYNGKSS 362
QY 372 ADDLKTGMPATEEVDICRLK 393
DB 363 ADDLRTNGVPATEEVDICRLK 384

RESULT 11

US-10-067-649-4
; Sequence 4, Application US/10067649
; Publication No. US20030100057A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY14, RELATED TO
; FILE REFERENCE: D0118 NP
; CURRENT APPLICATION NUMBER: US/10/067,649
; PRIOR FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2001-02-05
; PRIOR FILING DATE: 2001-02-05
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-067-649-4

Query Match 85.8%; Score 1764; DB 15; Length 393;
Best Local Similarity 84.0%; Pred. No. 1.2e-160;
Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 METTMGFMDDNATNTSTFSLVNLPHCAHATSPFNFYSYSDYDMPDLEDEDVTNSRTFFA 60
DB 1 METTVGALGENTDDTDFESALDGEAQTGSLPTFFESYDGYDMPDLEDEDVTNSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFPIALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFPIALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVRQLSWHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180
DB 121 DYVVRQLSWHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAA 180
QY 181 GLIALVMTVSIILAIAPSAVFTTETVLVIVKSOEIKFCGQIPWDOQLYKSYFLFIFGIE 240
DB 181 GLIFLVMSVSIILAIAPSAVFTTETVLVIVKSOEIKFCGQIPWDOQLYKSYFLFIFGIE 240
QY 241 FVGPVVTMLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPF 300
DB 241 FVGPVVTMLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPF 300
QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVKYFKKIMLH 360
DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVKYFKKIMLH 360
QY 361 WKASYNGKSSADLDTGMPATEEVDICRLK 393
DB 361 WRASPSGSKASADLDTGMPATEEVDICRLK 393

RESULT 12

US-09-764-556-2
; Sequence 2, Application US/09764556
; Patent No. US20020004222A1

; GENERAL INFORMATION:
; APPLICANT: ELISHOURBAGY, NABIL
; TITLE OF INVENTION: CLONING OF A MONKEY 7TM RECEPTOR (AXOR8)
; FILE REFERENCE: GP-70673
; CURRENT APPLICATION NUMBER: US/09/764,556
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: MACACA FASCICULARIS
US-09-764-556-2

Query Match 85.7%; Score 1762; DB 9; Length 384;
Best Local Similarity 87.4%; Pred. No. 1.9e-160;
Matches 334; Conservative 21; Mismatches 27; Indels 0; Gaps 0;

QY 12 ATNTSTFSLVNLPHCAHATSPFNFYSYSDYDMPDLEDEDVTNSRTFFA KIVIGMALVG 71
DB 3 AQNGTSTFAPNFPQDQHASLSFNSYDGYDLPDDEDEDVTNRTEFFA KIVIGIALAG 62
QY 72 IMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVVRQLSWE 131
DB 63 IMVCGIGNFVFAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVVRQLSWE 122
QY 132 HGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTATGLIALVMTVSI 191
DB 123 HGHVLCASVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTATGLIALVMTVSI 182
QY 192 LIAIPSAVFTTETVLVIVKSOEIKFCGQIPWDOQLYKSYFLFIFGIEFVGPVVTMLC 251
DB 183 LIAIPSAVFTETVLVIVKSOEIKFCGQIPWDOQLYKSYFLFIFGIEFVGPVVTMLC 242
QY 252 YARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGTIVRDFEP 311
DB 243 YARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGTIVRDFEP 302
QY 312 TVFVKEKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVKYFKKIMLHMKASYNGKSS 371
DB 303 TVFVKEKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVKYFKKIMLHMKASYNGKSS 362
QY 372 ADDLKTGMPATEEVDICRLK 393
DB 363 AELDRTNGVPATEEVDICRLK 384

RESULT 13

US-10-132-812-2
; Sequence 2, Application US/10132812
; Publication No. US20030059856A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Sarau, Henry M.
; APPLICANT: Slemmon, J. Randall
; APPLICANT: McNulty, Dean E.
; APPLICANT: Vawter, Lisa
; TITLE OF INVENTION: Methods Of Screening For Agonists And
; TITLE OF INVENTION: Agonists Of The Interaction Between The AXOR8 And AXOR52
; TITLE OF INVENTION: Receptors And Ligands Thereof
; FILE REFERENCE: PS1256
; CURRENT APPLICATION NUMBER: US/10/132,812
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,234
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 384

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: TYPE: PRT
: ORGANISM: Cercopithecus aethiops
US-10-132-812-2

Query Match      85.7%; Score 1762; DB 15; Length 384;
Best Local Similarity 87.4%; Pred. No. 1.9e-160;
Matches 334; Conservative 21; Mismatches 27; Indels 0; Gaps 0;

QY 12 ATNTSTFSLNPHGAHATSPFPNFSDYDMPDDEDEDTNSRTFFAAKIVIGMALVG 71
DB 3 AQNGNTSFAPNFPQDQDSSLSFNFSYGDYDLPDDEDEDTKTRFFAAKIVIGMALAG 62
QY 72 IMLVCGIGNFIFIAALVRYKKRLNLTLLIANLAISDFLVAIVCCPFENDYVYVRLSWE 131
DB 63 IMLVCGIGNFVFAALTRYKKRLNLTLLIANLAISDFLVAIVCCPFENDYVYVRLSWE 122
QY 132 HGHVLTCTSVNLTSLYSTNALLAIAIDRYLAIVHPLRPMKQATATGLIALVWTYSI 191
DB 123 HGHVLCASVNYLRTSVYSTNALLAIAIDRYLAIVHPLRPMYQOTASFLIALVWVSI 182
QY 192 LIAIPSAFYTTETVLVIVKQERIFCGQIWPVDQQLYKSYFLIFGIEFVGVPVVTMTLC 251
DB 183 LIAIPSAFYATETVLVIVKQERIFCGQIWPVDQQLYKSYFLIFGIEFVGVPVVTMTLC 242
QY 252 YARISRELWFKAVPGFQTEQIRKRLCRRTKRVTLVLMCILTAIVLWAPFYGFTIVRDFP 311
DB 243 YARISRELWFKAVPGFQTEQIRKRLCRRTKRVTLVLMCILTAIVLWAPFYGFTIVRDFP 302
QY 312 TVFVKEKHYLTATYVVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLHWKASYNGGKS 371
DB 303 TVFVKEKHYLTATYVVECIAMNSMINTVCFVTVKNTMKYFKKMLLHWRSQSGKS 362
QY 372 ADLDTLKTIGMPATEEVDICIRLK 393
DB 363 AELDLRTNGVPTTEEVDICIRLK 384

RESULT 14
US-10-220-289-5
: Sequence 5, Application US/10220289
: Publication No. US20030104435A1
: GENERAL INFORMATION:
: APPLICANT: Bayer AG
: TITLE OF INVENTION: REGULATION OF HUMAN SUBSTANCE P-LIKE G PROTEIN-COUPLED
: FILE REFERENCE: LA0010 Foreign Countries
: CURRENT APPLICATION NUMBER: US/10/220,289
: PRIOR FILING DATE: 2002-09-11
: PRIOR APPLICATION NUMBER: US 60/189,972
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 5
: LENGTH: 385
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-220-289-5

Query Match      85.48; Score 1755.5; DB 15; Length 385;
Best Local Similarity 87.24; Pred. No. 7.9e-160;
Matches 334; Conservative 20; Mismatches 28; Indels 1; Gaps 1;

QY 12 ATNTSTFSLNPHGAHATSPFPNFSDYDMPDDEDEDTNSRTFFAAKIVIGMALVG 71
DB 3 AQNGNTSFAPNFPQDQDSSLSFNFSYGDYDLPDDEDEDTKTRFFAAKIVIGMALAG 62
QY 72 IMLVCGIGNFIFIAALVRYKKRLNLTLLIANLAISDFLVAIVCCPFENDYVYVRLSWE 131
DB 63 IMLVCGIGNFVFAALTRYKKRLNLTLLIANLAISDFLVAIVCCPFENDYVYVRLSWE 122
QY 132 HGHVLTCTSVNLTSLYSTNALLAIAIDR-YLAIVHPLRPMKQATATGLIALVWVSI 190
DB 123 HGHVLCASVNYLRTSVYSTNALLAIAIDR-LAIVHPLKPRMYQOTASFLIALVWVSI 182

Query Match      82.94; Score 1703; DB 15; Length 355;
Best Local Similarity 90.14; Pred. No. 7.6e-155;
Matches 320; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 39 YSDYDMPDDEDEDTNSRTFFAAKIVIGMALVGMVCGIGNFIFIAALVRYKKRLNLTN 98
DB 1 YGDYDLPDDEDEDTKTRFFAAKIVIGMALVGMVCGIGNFIFIAALVRYKKRLNLTN 60
QY 99 LLIANLAISDFLVAIVCCPFENDYVYVRLSWEHGHVLTCTSVNLTSLYSTNALLAI 158
DB 61 LLIANLAISDFLVAIVCCPFENDYVYVRLSWEHGHVLTCTSVNLTSLYSTNALLAI 120
QY 159 AIDRYLAIVHPLRPMKQATATGLIALVWVSIILIAISATFTTETVLVIVKQEKIFCG 218
DB 121 AIDRYLAIVHPLKPRMYQOTASFLIALVWVSIILIAISATFATETVLVIVKQEKIFCG 180
QY 219 QIWPVDQQLYKSYFLIFGIEFVGVPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLRC 278
DB 181 QIWPVDQQLYKSYFLIFGIEFVGVPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLRC 240
QY 279 RRKTVLVLMCILTAIVLWAPFYGFTIVRDFPPTVFVEKHYLTAFYIVECIAMNSMIN 338
DB 241 RRKTVLVLMCILTAIVLWAPFYGFTIVRDFPPTVFVEKHYLTAFYIVECIAMNSMIN 300
QY 339 TFCFTVTVKNDTVKYFKKIMLLHWKASYNGGSSADLDTKTGHPATEEVDICIRLK 393
DB 301 TVCFVTVKNTMKYFKKMLLHWRSQSGSSADLDTKTGHPATEEVDICIRLK 355

Search completed: October 7, 2003, 10:01:54
Job time : 69 secs
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:48:57 ; Search time 44 Seconds
(without alignments)
1417.717 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTWGFMDDNATNTSTSL.....LDLKTIGMPATEVDCIRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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A_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------------------|
| 1 | 2055 | 100.0 | 393 | 22 | AAG62854 Amino acid sequenc |
| 2 | 2055 | 100.0 | 393 | 22 | AAG64121 Human G protein-co |
| 3 | 2055 | 100.0 | 393 | 22 | ABP81752 Human G protein-co |
| 4 | 2055 | 100.0 | 393 | 23 | ABG94396 Human GPCR protein |
| 5 | 2055 | 100.0 | 393 | 23 | ABB99157 Rat ZAQ protein. |
| 6 | 2055 | 100.0 | 393 | 23 | AAQ15524 Human physiologica |
| 7 | 2055 | 100.0 | 393 | 23 | ABB06955 Human ZAQ G protei |
| 8 | 2055 | 100.0 | 393 | 23 | ABR06303 Human ZAQ protein |
| 9 | 2035 | 99.0 | 389 | 21 | AAB03625 Human G-protein co |

| | | | | | | |
|----|--------|------|-----|----|----------|---------------------|
| 10 | 2035 | 99.0 | 389 | 22 | AAG62855 | Amino acid sequenc |
| 11 | 2035 | 99.0 | 389 | 24 | ABG76082 | Human G-protein co |
| 12 | 2035 | 99.0 | 389 | 24 | ABP81752 | Human G protein-co |
| 13 | 1924 | 93.6 | 382 | 23 | ABP76184 | Human G-protein co |
| 14 | 1767 | 86.0 | 393 | 23 | ABG94403 | Rat GPCR protein r |
| 15 | 1767 | 86.0 | 393 | 23 | ABB99158 | Rat ZAQ1 protein. |
| 16 | 1767 | 86.0 | 393 | 23 | ABB06953 | Rat ZAQ1 G protei |
| 17 | 1767 | 86.0 | 393 | 23 | ABB06312 | Human G protein-cou |
| 18 | 1766 | 85.9 | 384 | 19 | AAW79258 | Human G protein co |
| 19 | 1766 | 85.9 | 384 | 22 | AAU04362 | Human G-protein co |
| 20 | 1766 | 85.9 | 384 | 23 | ABG94405 | Human GPCR related |
| 21 | 1766 | 85.9 | 384 | 23 | ABB99161 | Human 15E. Homo s |
| 22 | 1766 | 85.9 | 384 | 23 | ABB06311 | Human 15E. Homo s |
| 23 | 1764 | 85.8 | 393 | 23 | ABG94406 | Mouse GPCR related |
| 24 | 1764 | 85.8 | 393 | 23 | ABB99162 | Mouse GPCR73. Mus |
| 25 | 1764 | 85.8 | 393 | 23 | ABB06314 | Mouse G protein-co |
| 26 | 1762 | 85.7 | 384 | 22 | AAU04635 | Monkey seven trans |
| 27 | 1755.5 | 85.4 | 385 | 22 | AAG78344 | Neuropeptide Y G p |
| 28 | 1755.5 | 85.4 | 385 | 22 | AAG78505 | Human mature SP-GP |
| 29 | 1715.5 | 83.5 | 421 | 23 | ABG94404 | Rat GPCR protein r |
| 30 | 1715.5 | 83.5 | 421 | 23 | ABB99159 | Rat ZAQ2 protein. |
| 31 | 1715.5 | 83.5 | 421 | 23 | ABB06954 | Rat ZAQ2 G protei |
| 32 | 1715.5 | 83.5 | 421 | 23 | ABB06313 | Rat G protein-cou |
| 33 | 1705 | 83.0 | 630 | 23 | AAE18651 | Human G-protein co |
| 34 | 1699.5 | 82.7 | 381 | 19 | AAW79259 | Mouse GPCR related |
| 35 | 1699.5 | 82.7 | 381 | 23 | ABG94407 | Mouse G protein co |
| 36 | 1699.5 | 82.7 | 381 | 23 | ABB99163 | Mouse GPCR related |
| 37 | 1699.5 | 82.7 | 381 | 23 | ABB06315 | Mouse M15E. Mus a |
| 38 | 1665.5 | 81.0 | 988 | 22 | ABG18888 | Mouse G protein-co |
| 39 | 1114 | 54.2 | 249 | 22 | ABG07211 | Novel human diagno |
| 40 | 1109 | 54.0 | 231 | 22 | AAG78343 | Neuropeptide Y G p |
| 41 | 1109 | 54.0 | 231 | 22 | AAG78504 | Human SP-GPCR exon |
| 42 | 1042 | 50.7 | 207 | 22 | AAG80945 | Human nGPCR34 #1. |
| 43 | 1042 | 50.7 | 207 | 23 | ABG93763 | Human G protein-co |
| 44 | 799 | 38.9 | 217 | 22 | AAG62847 | Amino acid sequenc |
| 45 | 657 | 32.0 | 153 | 22 | AAG78342 | Neuropeptide Y G p |

ALIGNMENTS

RESULT 1
AAG62854
ID AAG62854 standard; Protein; 393 AA.
XX
AC AAG62854;
XX
DT 17-SEP-2001 (first entry)
XX
XX Amino acid sequence of a G-protein coupled receptor.
XX
XX Human: G-protein coupled receptor; GPCR; thyroid disorder;
KW thyrotoxicosis; myxedema; renal failure; inflammatory condition;
KW Crohn's disease; arthritis; autoimmune disorder; stroke; migraine;
KW central nervous system disorder; pain; psychotic disorder;
KW anxiety disorder; post-traumatic-stress disorder; mania depression;
KW bipolar disorder; dementia; severe mental retardation;
KW Huntington's disease; degenerative disorder; Parkinson's; Alzheimer's;
KW infection; metabolic disorder; cardiovascular disease;
KW diabetes; obesity; anorexia; hypotension; hypertension; thrombosis;
KW myocardial infarction; atherosclerosis; proliferative disease; cancer;
KW hyperproliferative disorder; psoriasis; prostate hyperplasia;
KW hormonal disorder; polycystic ovarian syndrome.
XX
XX Homo sapiens.
OS
XX WO200148015-A2.
PN
XX
PD 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US35456.
XX

PR 28-DEC-1999; 99US-0173339.
 PR 23-FEB-2000; 2000US-0184305.
 PR 13-MAR-2000; 2000US-0188880.
 PR 27-APR-2000; 2000US-0200534.
 PR 20-JUL-2000; 2000US-0219492.
 PR 11-AUG-2000; 2000US-0224321.
 PR 09-OCT-2000; 2000US-0239062.
 XX (PHAA) PHARMACIA & UPJOHN CO.

XX Lind P, Parodi LA, Lindberg E, Vogell G, Wood LS, Hiebsch RR;
 PI Ruff V;

XX WPI: 2001-441707/47.
 DR N-PSDB; AAH42183.

XX G-protein coupled receptor (GPCR-x) nucleic acids and polypeptides
 PT encoded by them, useful for treating neurological and psychiatric
 PT disorders such as severe mental retardation, manic depression and
 PT dementia -

XX Example 1; Page 87; 175pp; English.

XX The present sequence represents human G-protein coupled receptor (GPCR).
 CC GPCRs may be used in the prevention, treatment and diagnosis of diseases
 CC associated with inappropriate GPCR expression such as thyroid disorders
 CC (e.g. thyrotoxicosis, myxedema), renal failure; inflammatory conditions
 CC (e.g., Crohn's disease); diseases related to cell differentiation and
 CC homeostasis; rheumatoid arthritis; autoimmune disorders; central
 CC nervous system (CNS) disorders (e.g., pain including migraine; stroke;
 CC psychotic and neurological disorders such as anxiety, mental disorder,
 CC manic depression, generalized anxiety disorder, post-traumatic-stress
 CC disorder, depression, bipolar disorder, dementia, severe mental
 CC retardation; Huntington's disease; degenerative disorders such as
 CC Parkinson's, Alzheimer's; infections such as viral infections caused by
 CC HIV-1 or HIV-2; metabolic and cardiovascular disease and disorders
 CC (e.g., type 2 diabetes, obesity, anorexia, hypotension, hypertension,
 CC thrombosis, myocardial infarction, atherosclerosis); proliferative
 CC diseases and cancers and hyperproliferative disorders such as
 CC psoriasis, prostate hyperplasia); hormonal disorders (male/female
 CC hormonal replacement, polycystic ovarian syndrome).

XX Sequence 393 AA;

Query Match 100.0%; Score 2055; DB 22; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTGMFDDNATNTSTSLVNLNPHGHAHATSPFNFSYSDYDMPLEDEEDVTSRTFFA 60

DB 1 METTGMFDDNATNTSTSLVNLNPHGHAHATSPFNFSYSDYDMPLEDEEDVTSRTFFA 60

QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120

DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120

QY 121 DYVVVROLSWEHGHVLTCTSVNYLRTVSLVSNALLAIAIDRYLAIVHPLRPMKQAT 180

DB 121 DYVVVROLSWEHGHVLTCTSVNYLRTVSLVSNALLAIAIDRYLAIVHPLRPMKQAT 180

QY 181 GLIALVMTVSLIIAIPSAVFTTETVLVIVKSOEKFICGQIWPVDQOLYKYSFLFIFGIE 240

DB 181 GLIALVMTVSLIIAIPSAVFTTETVLVIVKSOEKFICGQIWPVDQOLYKYSFLFIFGIE 240

QY 241 FVGPVVMTLCYARIISRELWFAVPGFQEQIKRLRCRRKTVLVLMCLTATVLCWAPF 300

DB 241 FVGPVVMTLCYARIISRELWFAVPGFQEQIKRLRCRRKTVLVLMCLTATVLCWAPF 300

QY 301 YGFTIVRDPFPTVVKKKHYLTAFYIIVECIANSNMINTLCFTVKNADVYKFKIMLLH 360

DB 301 YGFTIVRDPFPTVVKKKHYLTAFYIIVECIANSNMINTLCFTVKNADVYKFKIMLLH 360

QY 361 WKASYNNGKSSADLDLKTIGMPATEEVDICRLK 393

DB 361 WKASYNNGKSSADLDLKTIGMPATEEVDICRLK 393

RESULT 2

AAAG64121

ID AAG64121 standard; Protein; 393 AA.

XX AAG64121;

XX 25-SEP-2001 (first entry)

XX Human G protein-coupled receptor GPRV21.

XX Human; guanosine triphosphate binding protein-coupled receptor;
 KW G-protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;
 KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;
 KW Alzheimer's disease; cytostatic; hepatotropic; nootropic;
 KW neuroprotective; gene therapy; peptide therapy.

XX Homo sapiens.

XX WO200148188-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-JP09408.

XX 28-DEC-1999; 99JP-0375152.

XX 31-MAR-2000; 2000JP-0101339.

XX (HEL1-) HELIX RES INST.

PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
 PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;

XX WPI: 2001-425662/45.

XX N-PSDB; AAH73504.

XX New DNA encoding guanosine triphosphate binding protein coupled
 PT receptors and their expression products for screening potential
 PT anticancer and nootropic drugs and in diagnosis of these diseases -

XX Claim 1; Page 111-114; 170pp; Japanese.

XX The invention relates to nine human guanosine triphosphate binding
 CC protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,
 CC GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the
 CC genes encoding them. These genes and proteins and antibodies against
 CC the protein are useful in the treatment, prevention, diagnosis and
 CC investigation of diseases associated with G protein-coupled receptors,
 CC including cancer, cirrhosis of the liver and Alzheimer's disease.
 CC The present sequence is a G protein-coupled receptor of the invention.

XX Sequence 393 AA;

Query Match 100.0%; Score 2055; DB 22; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTGMFDDNATNTSTSLVNLNPHGHAHATSPFNFSYSDYDMPLEDEEDVTSRTFFA 60

DB 1 METTGMFDDNATNTSTSLVNLNPHGHAHATSPFNFSYSDYDMPLEDEEDVTSRTFFA 60

QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120

DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120

QY 121 DYVVVROLSWEHGHVLTCTSVNYLRTVSLVSNALLAIAIDRYLAIVHPLRPMKQAT 180

DB 121 DYVVVROLSWEHGHVLTCTSVNYLRTVSLVSNALLAIAIDRYLAIVHPLRPMKQAT 180

QY 181 GLIALVMTVSLIIAIPSAVFTTETVLVIVKSOEKFICGQIWPVDQOLYKYSFLFIFGIE 240

181 GLIALVWTVSILIAIPSAFTTETVLIVKSGEIKFCGQWPDQQLYKSYELFIFGIE 240
 241 FVGPPVTMTLCYARISRELWFKAVPGFQTOIRKRLCRKRTVLVLMCILTAYVLCWAPF 300
 241 FVGPPVTMTLCYARISRELWFKAVPGFQTOIRKRLCRKRTVLVLMCILTAYVLCWAPF 300
 301 YGFTIVRDFPFTVVKKKHYLTAFYIIVECIAMNSMINTLCFTVKNKDYVKYFKKIMLLH 360
 301 YGFTIVRDFPFTVVKKKHYLTAFYIIVECIAMNSMINTLCFTVKNKDYVKYFKKIMLLH 360
 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393

RESULT 3
 AAB70143
 ID AAB70143 standard; protein; 393 AA.
 XX AC AAB70143;
 XX DT 29-MAY-2001 (first entry)
 XX DE Human G protein-coupled receptor protein.
 XX KW Human; G protein-coupled receptor protein; nootropic; neuroprotective;
 KW hypotensive; orexigenic; anti-allergic; anti-anginal; antimicrobial;
 KW antibacterial; gene therapy; Alzheimer's disease; hypertension;
 KW anorexia; allergy; angina pectoris; infection; MRSA;
 KW multiple resistant Staphylococcus aureus.
 XX OS Homo sapiens.
 XX PN WO200116309-A1.
 XX PD 08-MAR-2001.
 XX PF 24-ACG-2000; 2000WO-JP05685.
 XX PR 27-AUG-1999; 95JP-0241531.
 PR 18-JUL-2000; 2000JP-0217474.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Watanabe T, Terao Y, Shintani Y;
 XX WPI; 2001-226684/23.
 DR N-PSDB; AAF79501.
 XX PT New human brain-originated guanosine triphosphate protein-coupled
 PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
 PT and development of preventives and remedies for Alzheimer's disease,
 PT hypertension and anorexia -
 XX PS Claim 1; Fig 1-3; 119pp; Japanese.
 XX CC The present sequence is provided in a specification relating to a
 CC protein or its salt with an amino acid sequence identical or
 CC substantially similar to a fully defined sequence of 393 amino acids as
 CC given in the specification. The protein is useful in gene diagnosis and
 CC development of preventives and remedies for diseases associated with
 CC dysfunction of the protein, e.g. Alzheimer's disease, hypertension,
 CC anorexia, allergy, angina pectoris and infections (e.g. multiple
 CC resistant Staphylococcus aureus). The proteins and DNA encoding the
 CC proteins are also useful for the treatment of these diseases by gene
 CC therapy.
 XX SQ Sequence 393 AA;

Query Match 100.0%; Score 2055; DB 22; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.7e-27;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFESYSDYDMPDDEDEDVTSRTFFA 60
 DB 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFESYSDYDMPDDEDEDVTSRTFFA 60
 QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
 DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
 QY 121 DYVVVQLSWEHGHVLTCTSVNLTSLVSYSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180
 DB 121 DYVVVQLSWEHGHVLTCTSVNLTSLVSYSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180
 QY 181 GLIALVWTVSILIAIPSAFTTETVLIVKSGEIKFCGQWPDQQLYKSYELFIFGIE 240
 DB 181 GLIALVWTVSILIAIPSAFTTETVLIVKSGEIKFCGQWPDQQLYKSYELFIFGIE 240
 QY 241 FVGPPVTMTLCYARISRELWFKAVPGFQTOIRKRLCRKRTVLVLMCILTAYVLCWAPF 300
 DB 241 FVGPPVTMTLCYARISRELWFKAVPGFQTOIRKRLCRKRTVLVLMCILTAYVLCWAPF 300
 QY 301 YGFTIVRDFPFTVVKKKHYLTAFYIIVECIAMNSMINTLCFTVKNKDYVKYFKKIMLLH 360
 DB 301 YGFTIVRDFPFTVVKKKHYLTAFYIIVECIAMNSMINTLCFTVKNKDYVKYFKKIMLLH 360
 QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
 DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393

RESULT 4
 ABG94396
 ID ABG94396 standard; protein; 393 AA.
 XX AC ABG94396;
 XX DT 27-NOV-2002 (first entry)
 XX DE Human GPCR protein ZAQ.
 XX KW G-protein coupled receptor; GPCR; ZAQ; human; ZAQ; ZAQ; rat; ZAQ;
 KW rZAQ1; rZAQ2; mouse; 15E receptor; m15E; GPR73; Bv8 protein; MIT1;
 KW digestive disorder; central nervous system disorder; CNS; diarrhoea;
 KW bowel inflammation; constipation; food absorption disorder; nootropic;
 KW Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;
 KW anti-inflammatory; antidiarrhoeic; neuroleptic; neuroprotective;
 KW receptor.
 XX OS Homo sapiens.
 XX PN WO200262944-A2.
 XX PD 15-AUG-2002.
 XX PF 01-FEB-2002; 2002WO-JP00852.
 XX PR 02-FEB-2001; 2001JP-0026820.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
 PI Hinuma S;
 DR WPI; 2002-627537/67.
 DR N-PSDB; ABS71088.
 XX PT Screening of compounds modifying the binding of G-protein coupled
 PT receptor protein ZAQ and related proteins to their ligands for use in
 PT treatment and diagnosis of digestive disorders -
 XX PS Claim 1; Fig 1-3; 197pp; Japanese.
 XX CC The present invention relates to a screening method for compounds

CC for their ability to modify the binding of G-protein coupled receptor
 CC (GPCR) protein ZAQ and related proteins (human ZAQ, human ZAQ1,
 CC rat ZAQ1 (rZAQ1), rZAQ2, human and mouse ISE (mISE) receptor, and
 CC mouse GPR73) to their ligands (the mature form of human, mouse or rat
 CC bV8 protein). The receptor protein and ligand are contacted in the
 CC presence or absence of the test compound. The compounds are useful
 CC in a drug composition for the treatment, and prevention of digestive
 CC and central nervous system (CNS) disorders, including bowel
 CC inflammation, diarrhoea, constipation, food absorption disorders,
 CC Alzheimer's disease, Parkinson's disease and schizophrenia.
 CC The present sequence represents a GPCR or related protein.
 XX
 SQ Sequence 393 AA;

Query Match 100.0%; Score 2055; DB 23; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTMGFMDNATNTSTSLVLPNPHGHAHATSPFPNFSDYDMPLEDEDEVTNSRTFFA 60
 DB 1 METTMGFMDNATNTSTSLVLPNPHGHAHATSPFPNFSDYDMPLEDEDEVTNSRTFFA 60

QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
 DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120

QY 121 DYVVVROLSEHGHLVCTSVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180
 DB 121 DYVVVROLSEHGHLVCTSVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180

QY 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSKIFCGQIWPVDOOLYKSYFLFIGIE 240
 DB 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSKIFCGQIWPVDOOLYKSYFLFIGIE 240

QY 241 FVGPVVTMTLCYARISRELWFKAVPGFQTEOIRKRLCRKRTVLLVLMCILTAYVLCWAPF 300
 DB 241 FVGPVVTMTLCYARISRELWFKAVPGFQTEOIRKRLCRKRTVLLVLMCILTAYVLCWAPF 300

QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFTVTKNDTVKFKKIMLH 360
 DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFTVTKNDTVKFKKIMLH 360

QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
 DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393

RESULT 5
 ABB99157
 ID ABB99157 standard; Protein; 393 AA.
 XX
 AC ABB99157;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Rat ZAQ protein.
 XX
 KW Rat; physiological; G protein-coupled receptor; ZAQ; antidiarrheic;
 KW laxative; anti-inflammatory; digestive disease; diarrhoea; constipation;
 KW colitis; gene therapy.
 XX
 XX Rattus sp.
 XX
 PN WO200262996-A1.
 XX
 PD 15-AUG-2002.
 XX
 PF 01-FEB-2002; 2002WO-JP00837.
 XX
 PR 02-FEB-2001; 2001JP-0026798.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PD 25-JUL-2002.

PI Ohtaki T, Masuda Y, Takatsu Y;
 XX WPI; 2002-627554/67.
 DR N-PSDB; ABQ9083, ABQ9084.
 XX
 PT Physiologically-active brain-originated G protein-coupled receptor
 PT peptide ZAQ and encoding DNA, useful for developing drugs to treat
 PT digestive diseases e.g. diarrhoea, constipation and colitis, including
 PT gene therapy -
 XX
 FS Claim 16; Fig 1-3; 184pp; Japanese.
 XX
 CC The invention relates to a novel physiologically-active brain-originated
 CC G protein-coupled receptor peptide designated ZAQ. The proteins of the
 CC invention have antidiarrheic, laxative, and anti-inflammatory activity.
 CC The DNA and encoded protein are useful for developing drugs for the
 CC treatment of diseases of the digestive organs e.g. diarrhoea,
 CC constipation and colitis. The polynucleotides may have a use in gene
 CC therapy. The sequence represents a rat ZAQ protein of the invention.
 XX
 SQ Sequence 393 AA;

Query Match 100.0%; Score 2055; DB 23; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTMGFMDNATNTSTSLVLPNPHGHAHATSPFPNFSDYDMPLEDEDEVTNSRTFFA 60
 DB 1 METTMGFMDNATNTSTSLVLPNPHGHAHATSPFPNFSDYDMPLEDEDEVTNSRTFFA 60

QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
 DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120

QY 121 DYVVVROLSEHGHLVCTSVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180
 DB 121 DYVVVROLSEHGHLVCTSVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180

QY 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSKIFCGQIWPVDOOLYKSYFLFIGIE 240
 DB 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSKIFCGQIWPVDOOLYKSYFLFIGIE 240

QY 241 FVGPVVTMTLCYARISRELWFKAVPGFQTEOIRKRLCRKRTVLLVLMCILTAYVLCWAPF 300
 DB 241 FVGPVVTMTLCYARISRELWFKAVPGFQTEOIRKRLCRKRTVLLVLMCILTAYVLCWAPF 300

QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFTVTKNDTVKFKKIMLH 360
 DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFTVTKNDTVKFKKIMLH 360

QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
 DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393

RESULT 6
 AAO15524
 ID AAO15524 standard; Protein; 393 AA.
 XX
 AC AAO15524;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Human physiologically-active ZAQ ligand-related protein 1.
 XX
 KW Human; ZAQ ligand; physiologically-active ZAQ ligand;
 KW digestive disease; colitis; diarrhoea.
 XX
 OS Homo sapiens.
 XX
 PN WO200257443-A1.
 XX
 PD 25-JUL-2002.

XX 21-JAN-2002; 2002WO-JP00378.
XX
XX
PR 22-JAN-2001; 2001JP-0013027.
PR 17-MAY-2001; 2001JP-0147759.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Yamada T, Suenaga M, Nishimura O;
XX WPI; 2002-566801/60.
DR
XX
XX Industrial production of physiologically-active ZAQ ligand by
PT expressing in transformant prokaryote and refolding in redox buffer,
PT for use in preventing or treating digestive diseases e.g. colitis and
PT diarrhea
XX
XX Claim 1; Page 66-68; 93pp; Japanese.
XX
XX The invention comprises a method for producing an active peptide that has
CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
CC method of the invention is useful for the production of a
CC physiologically-active ZAQ ligand for use in preventing or treating
CC digestive diseases (e.g. colitis and diarrhea). The present amino acid
CC sequence represents a human physiologically active ZAQ ligand-related
CC protein.
XX
XX Sequence 393 AA;
XX
Query Match 100.0%; Score 2055; DB 23; Length 393;
Best Local Similarity 100.0%; Pred. No. 3.7e-227;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METTMGFDDNATNTSTSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTNSRTFFA 60
DB 1 METTMGFDDNATNTSTSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTNSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180
DB 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180
QY 181 GLIALVMTVTSILIAIPSAFTTETVLVIVKSOEKIFCGIWPVDQOLYKSYFLFIFGIE 240
DB 181 GLIALVMTVTSILIAIPSAFTTETVLVIVKSOEKIFCGIWPVDQOLYKSYFLFIFGIE 240
QY 241 FVGPPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTATVLCWAPF 300
DB 241 FVGPPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTATVLCWAPF 300
QY 301 YGFTIVRDEFPPTVVKKEHYLTAFYIVECIAMNSMINTLCFTVVKNDTVKYFKKIMLLH 360
DB 301 YGFTIVRDEFPPTVVKKEHYLTAFYIVECIAMNSMINTLCFTVVKNDTVKYFKKIMLLH 360
QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
RESULT 7
ABB06955
ID ABB06955 standard; Protein; 393 AA.
XX
AC ABB06955;
XX
DT 19-JUN-2002 (first entry)
XX
DE Human ZAQ G protein-coupled receptor protein SEQ ID NO:12.
XX
KW Human; rZAQ1; rZAQ2; G protein-coupled receptor; GPCR; antidiarrheic;

KW laxative; drug development; digestive organ disease; colitis; diarrhoea;
KW constipation; malabsorption syndrome; diagnosis; gene therapy.
XX Homo sapiens.
OS
PN WO200216607-A1.
XX
PO 28-FEB-2002.
XX
XX 23-AUG-2001; 2001WO-JP07209.
XX
PR 24-AUG-2000; 2000JP-0253862.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Teraso Y, Shintani Y;
XX
XX WPI; 2002-269361/31.
XX
XX Human and rat brain-originated G protein-coupled receptor proteins and
PT encoded DNAs, for developing drugs to treat diseases of the digestive
CC organs, e.g. colitis, diarrhea, constipation and mal-absorption
PT syndrome
XX
XX Example 1; Page 101-102; 135pp; Japanese.
XX
XX The present invention describes human and rat brain-originated
CC G protein-coupled receptor (GPCR) proteins. The GPCR sequences have
CC antidiarrheic and laxative activities. The GPCR sequences can be used
CC for developing drugs to treat diseases of the digestive organs,
CC e.g. colitis, diarrhoea, constipation and malabsorption syndrome,
CC including gene diagnosis and therapy. The present sequence represents
CC a human GPCR designated ZAQ, which is given in the present invention.
XX
XX Sequence 393 AA;
XX
Query Match 100.0%; Score 2055; DB 23; Length 393;
Best Local Similarity 100.0%; Pred. No. 3.7e-227;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METTMGFDDNATNTSTSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTNSRTFFA 60
DB 1 METTMGFDDNATNTSTSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTNSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180
DB 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180
QY 181 GLIALVMTVTSILIAIPSAFTTETVLVIVKSOEKIFCGIWPVDQOLYKSYFLFIFGIE 240
DB 181 GLIALVMTVTSILIAIPSAFTTETVLVIVKSOEKIFCGIWPVDQOLYKSYFLFIFGIE 240
QY 241 FVGPPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTATVLCWAPF 300
DB 241 FVGPPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTATVLCWAPF 300
QY 301 YGFTIVRDEFPPTVVKKEHYLTAFYIVECIAMNSMINTLCFTVVKNDTVKYFKKIMLLH 360
DB 301 YGFTIVRDEFPPTVVKKEHYLTAFYIVECIAMNSMINTLCFTVVKNDTVKYFKKIMLLH 360
QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
RESULT 8
ABB06303
ID ABB06303 standard; Protein; 393 AA.
XX

AC ABB06303;
 XX 27-MAY-2002 (first entry)
 XX Human ZAQ protein sequence SEQ ID NO:1.
 XX G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
 KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;
 KW colitis; diarrhoea; constipation; poor-absorption syndrome;
 KW gene therapy.
 XX Homo sapiens.
 OS WO200206483-A1.
 PN 24-JAN-2002.
 PD 17-JUL-2001; 2001WO-JP06162.
 PF 18-JUL-2000; 2000JP-0217442.
 PR 02-FEB-2001; 2001JP-0026779.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
 PI Hinuma S;
 PI WPI: 2002-188546/24.
 DR N-PSDB: ABL49615, ABL49616.
 XX Physiologically-active peptides from cows milk, useful for developing
 PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
 PT like colitis, diarrhoea, constipation and poor-absorption syndrome, by
 PT gene therapy
 XX Claim 14; Page 51-52; 191pp; Japanese.
 XX The present invention describes a peptide containing an amino acid
 CC sequence (I) identical to or substantially similar to that of the
 CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic
 CC and laxative activities. The peptides and encoding DNAs from the
 CC present invention are useful for developing drugs to treat digestive
 CC diseases like colitis, diarrhoea, constipation and poor-absorption
 CC syndrome, including gene therapy. the physiologically-active cows
 CC milk-originated peptides are applicable as a specific ligand of
 CC brain-originated orphan G protein-coupled receptor protein ZAQ.
 CC ABL49615 to ABB40659 and ABB06303 to ABB06315 represent sequences
 CC used in the exemplification of the present invention.
 XX Sequence 393 AA;
 SQ Query Match 100.0%; Score 2055; DB 23; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 M E T T M G F M D N A T W T S F L S V L N P H G A H A T S F P F N F S Y S D Y D M P L D E D E D V T N S R T F F A 60
 DB 1 M E T T M G F M D N A T W T S F L S V L N P H G A H A T S F P F N F S Y S D Y D M P L D E D E D V T N S R T F F A 60
 QY 61 A K I V I G M A L V G I M L V C G I G N F I F I A A L V R Y K K L R N L T N L I A N L A I S D F L V A I V C C P F E M 120
 DB 61 A K I V I G M A L V G I M L V C G I G N F I F I A A L V R Y K K L R N L T N L I A N L A I S D F L V A I V C C P F E M 120
 QY 121 D Y Y V V R Q L S W E H G V L C T S V N Y L T V S L Y S T N A L L A I A I D R Y L A I V H P L R P M K C Q T A T 180
 DB 121 D Y Y V V R Q L S W E H G V L C T S V N Y L T V S L Y S T N A L L A I A I D R Y L A I V H P L R P M K C Q T A T 180
 QY 181 G L I A L W T V S I L I A P S A Y F T T E T V L V I V K S Q E K I F C G Q I W P V D Q Q L Y K S Y F L F I G I E 240
 DB 181 G L I A L W T V S I L I A P S A Y F T T E T V L V I V K S Q E K I F C G Q I W P V D Q Q L Y K S Y F L F I G I E 240
 QY 241 F V G P V V T M T L C Y A R I S R E L W F K A V P G F Q T E I R K R L C R R K T V L V L M C I L T A Y V L C W A P F 300
 DB 241 F V G P V V T M T L C Y A R I S R E L W F K A V P G F Q T E I R K R L C R R K T V L V L M C I L T A Y V L C W A P F 300

Db 241 F V G P V V T M T L C Y A R I S R E L W F K A V P G F Q T E I R K R L C R R K T V L V L M C I L T A Y V L C W A P F 300
 QY 301 Y G F T I V R D F P P T V F V K E K H Y L T A F Y I V E C T A N S N S M I N T L C F V T V K N D T V K Y F K K I M L L H 360
 Db 301 Y G F T I V R D F P P T V F V K E K H Y L T A F Y I V E C T A N S N S M I N T L C F V T V K N D T V K Y F K K I M L L H 360
 QY 361 W K A S Y N G K S S A D L D L K T I G M P A T E E V D C I R L K 393
 Db 361 W K A S Y N G K S S A D L D L K T I G M P A T E E V D C I R L K 393
 RESULT 9
 AAB03625
 ID AAB03625 standard; Protein; 389 AA.
 XX AAB03625;
 AC AAB03625;
 DT 03-JAN-2001 (first entry)
 XX Human G-protein coupled receptor fb41a.
 DE Human; fb41a; G-protein coupled receptor; memory loss; depression;
 KW anxiety; epilepsy; pain; hypertension; locomotor problems;
 KW circadian rhythm disorder; eating/body weight disorder;
 KW sexual/reproductive disorder; nasal congestion; diarrhoea;
 KW gastrointestinal disorder; cardiovascular disorder.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Domain 58..84 /label= potential_transmembrane_region
 FT Domain 95..117 /label= potential_transmembrane_region
 FT Domain 136..156 /label= potential_transmembrane_region
 FT Domain 175..196 /label= potential_transmembrane_region
 FT Domain 228..249 /label= potential_transmembrane_region
 FT Domain 282..305 /label= potential_transmembrane_region
 FT Domain 319..341 /label= potential_transmembrane_region
 FT Domain /label= potential_transmembrane_region
 XX WO200034334-A1.
 PN 15-JUN-2000.
 PD 10-DEC-1999; 99WO-US29268.
 PF 10-DEC-1998; 98US-0210279.
 PR (SYNA-) SYNAPTIC PHARM CORP.
 PA Bard JA;
 PI WPI: 2000-431277/37.
 DR N-PSDB: AAA53210.
 XX Novel nucleic acid encoding a mammalian fb41a receptor useful for
 PT treating hypertension, diabetes, asthma, obesity and gastrointestinal
 PT disorders
 XX Claim 9; Fig 2; 133pp; English.
 CC The present sequence is the protein sequence for the human fb41a
 CC G-protein coupled receptor. This protein is a neuroregulator and is
 CC involved in communication within the nervous system. Its coding sequence
 CC was isolated by screening a human placental genomic DNA library for
 CC sequences similar to that encoding WPI4. The gene and protein can be
 CC used to treat the following types of disorder: those involving the
 CC regulation of steroid hormones, epinephrine release, the

CC gastrointestinal tract, the cardiovascular system, electrolyte
 CC balance, hypertension, diabetes, respiration, asthma, reproductive
 CC function, the immune system, endocrine function, the musculoskeletal
 CC system, visceral innervation, neuroendocrine function, cognition, sensory
 CC memory, sensory modulation and transmission, motor coordination, sensory
 CC integration, motor integration, dopaminergic function, appetite,
 CC obesity, olfaction, sympathetic innervation or migraine.
 XX Sequence 389 AA;
 SQ

Query Match 99.0%; Score 2035; DB 21; Length 389;
 Best Local Similarity 100.0%; Pred. No. 7.3e-225;
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 MGFDDNATNTSTFSLVLPNGAHATSPFNFYSYSDYDPLDEDEDTNSRTFFAAKIV 64
 Dd 1 MGFDDNATNTSTFSLVLPNGAHATSPFNFYSYSDYDPLDEDEDTNSRTFFAAKIV 60
 Qy 65 IGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEMDYV 124
 Dd 61 IGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEMDYV 120
 Qy 125 VROLSEHGHLVCTSVNYLRTVSVLTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA 184
 Dd 121 VROLSEHGHLVCTSVNYLRTVSVLTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA 180
 Qy 185 LVWTVSILAIAPSAFTTETVLVIVKSOEIKFCQIWPVQDQLYKSYFLFIEFVGP 244
 Dd 181 LVWTVSILAIAPSAFTTETVLVIVKSOEIKFCQIWPVQDQLYKSYFLFIEFVGP 240
 Qy 245 VVTMTLCYARISRELWFAVPGFQEQIRKRLCRRTVLVLMCILTAIYVLCWAPFYGT 304
 Dd 241 VVTMTLCYARISRELWFAVPGFQEQIRKRLCRRTVLVLMCILTAIYVLCWAPFYGT 300
 Qy 305 IVRDFPTFVFEKHHYLTAFYIVCEIAMSNSMINTLCFTVVKNDTVYFKKIMLLHWKAS 364
 Dd 301 IVRDFPTFVFEKHHYLTAFYIVCEIAMSNSMINTLCFTVVKNDTVYFKKIMLLHWKAS 360
 Qy 365 YNGKSSADLLKTIGMPATEVDCIRLK 393
 Dd 361 YNGKSSADLLKTIGMPATEVDCIRLK 389

RESULT 10
 AAG62855
 ID AAG62855 standard; Protein: 389 AA.
 XX
 AC AAG62855;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Amino acid sequence of a G-protein coupled receptor.
 XX
 KW Human; G-protein coupled receptor; GPCR; thyroid disorder;
 KW thyrotoxicosis; myxedema; renal failure; inflammatory condition;
 KW Crohn's disease; arthritis; autoimmune disorder; stroke; migraine;
 KW central nervous system disorder; pain; psychotic disorder;
 KW neurological disorder; anxiety; mental disorder; manic depression;
 KW anxiety disorder; post-traumatic-stress disorder; depression;
 KW bipolar disorder; dementia; severe mental retardation;
 KW Huntington's disease; degenerative disorder; Parkinson's; Alzheimer's;
 KW infection; metabolic disorder; cardiovascular disease;
 KW diabetes; obesity; anorexia; hypotension; hypertension; thrombosis;
 KW myocardial infarction; atherosclerosis; proliferative disease; cancer;
 KW hyperproliferative disorder; psoriasis; prostate hyperplasia;
 KW hormonal disorder; polycystic ovarian syndrome.
 XX
 OS Homo sapiens.
 XX
 PN W0200148015-A2.
 XX
 PD 05-JUL-2001.
 XX

PF 28-DEC-2000; 2000MO-US35456.
 XX 28-DEC-1999; 99US-0173339.
 PR 23-FEB-2000; 2000US-0184305.
 PR 13-MAR-2000; 2000US-0188880.
 PR 27-APR-2000; 2000US-0200534.
 PR 20-JUL-2000; 2000US-0219492.
 PR 11-AUG-2000; 2000US-0224321.
 PR 09-OCT-2000; 2000US-0239062.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Lind P, Parodi LA, Lindberg E, Vogeli G, Wood LS, Hiebsch RR;
 PI Ruff V;
 XX WPI; 2001-441707/47.
 DR N-PSDB; AAH42183.
 XX
 PT G-protein coupled receptor (GPCR-x) nucleic acids and polypeptides
 PT encoded by them, useful for treating neurological and psychiatric
 PT disorders such as severe mental retardation, manic depression and
 PT dementia -
 XX
 PS Example 1; Page 87; 175pp; English.
 XX
 CC The present sequence represents human G-protein coupled receptor (GPCR).
 CC GPCRs may be used in the prevention, treatment and diagnosis of diseases
 CC associated with inappropriate GPCR expression such as thyroid disorders
 CC (e.g. thyrotoxicosis, myxedema), renal failure; inflammatory conditions
 CC (e.g., Crohn's disease); diseases related to cell differentiation and
 CC homeostasis; rheumatoid arthritis; autoimmune disorders; central
 CC nervous system (CNS) disorders (e.g., pain including migraine; stroke;
 CC psychotic and neurological disorders such as anxiety, mental disorder,
 CC manic depression, generalized anxiety disorder, post-traumatic-stress
 CC disorder, depression, bipolar disorder, dementia, severe mental
 CC retardation; Huntington's disease; degenerative disorders such as
 CC Parkinson's, Alzheimer's; infections such as viral infections caused by
 CC HIV-1 or HIV-2; metabolic and cardiovascular disease and disorders
 CC (e.g., type 2 diabetes, obesity, anorexia, hypotension, hypertension,
 CC thrombosis, myocardial infarction, atherosclerosis); proliferative
 CC diseases and cancers and hyperproliferative disorders such as
 CC psoriasis, prostate hyperplasia); hormonal disorders (male/female
 CC hormonal replacement, polycystic ovarian syndrome).
 XX
 SQ Sequence 389 AA;
 Query Match 99.0%; Score 2035; DB 22; Length 389;
 Best Local Similarity 100.0%; Pred. No. 7.3e-225;
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 MGFDDNATNTSTFSLVLPNGAHATSPFNFYSYSDYDPLDEDEDTNSRTFFAAKIV 64
 Dd 1 MGFDDNATNTSTFSLVLPNGAHATSPFNFYSYSDYDPLDEDEDTNSRTFFAAKIV 60
 Qy 65 IGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEMDYV 124
 Dd 61 IGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEMDYV 120
 Qy 125 VROLSEHGHLVCTSVNYLRTVSVLTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA 184
 Dd 121 VROLSEHGHLVCTSVNYLRTVSVLTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA 180
 Qy 185 LVWTVSILAIAPSAFTTETVLVIVKSOEIKFCQIWPVQDQLYKSYFLFIEFVGP 244
 Dd 181 LVWTVSILAIAPSAFTTETVLVIVKSOEIKFCQIWPVQDQLYKSYFLFIEFVGP 240
 Qy 245 VVTMTLCYARISRELWFAVPGFQEQIRKRLCRRTVLVLMCILTAIYVLCWAPFYGT 304
 Dd 241 VVTMTLCYARISRELWFAVPGFQEQIRKRLCRRTVLVLMCILTAIYVLCWAPFYGT 300
 Qy 305 IVRDFPTFVFEKHHYLTAFYIVCEIAMSNSMINTLCFTVVKNDTVYFKKIMLLHWKAS 364
 Dd 301 IVRDFPTFVFEKHHYLTAFYIVCEIAMSNSMINTLCFTVVKNDTVYFKKIMLLHWKAS 360

QY 365 YNGKSSADLDLKTIGMPATEVDCIRLK 393
|||||
DB 361 YNGKSSADLDLKTIGMPATEVDCIRLK 389
RESULT 11
ID ABG76082 standard; Protein; 389 AA.
XX
AC ABG76082;
XX
DT 09-MAY-2003 (first entry)
XX
DE Human G-protein coupled receptor fb41a.
XX
KW Human; fb41a; GPCR; G-protein coupled receptor; immune disorder;
KW fb41a associated disorder; steroid hormone regulation; appetite;
KW epinephrine release; gastrointestinal disorder; reproductive disorder;
KW endocrine disorder; musculoskeletal disorder; visceral innervation
KW neuroendocrine disorder; cognitive disorder; motor coordination;
KW memory; sensory modulation; sensory transmission; sensory integration;
KW motor integration; dopaminergic function; olfaction; hypertension;
KW sympathetic innervation; cardiovascular disorder; respiratory disorder;
KW electrolyte balance disorder; diabetes; asthma; migraine.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 4..389
FT /label= Truncated_fb41a
FT /note= "This is the truncated form of fb41a
FT encoded by ABX11940".
XX
PN US2002165380-A1.
XX
PD 07-NOV-2002...
XX
PF 09-AUG-2001; 2001US-0925922.
XX
PR 10-DEC-1998; 98US-0210279.
XX
PA (BARD/) BARD J A.
PI Bard JA;
XX
XX WPI; 2003-288148/28.
DR N-PSDB; ABX11940.
XX
PT New isolated human fb41a receptor nucleic acid, useful for the
PT diagnosis, prevention or treatment of disorders with aberrant
PT expression or activity of the fb41a receptor protein, such as
PT hypertension, diabetes, asthma and migraine.
XX
PS Claim 9; Fig 2; 40pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a mammalian
CC G-protein coupled receptor, fb41a. The methods and compositions of the
CC present invention are useful for the diagnosis, prevention and/or
CC treatment of disorders associated with aberrant expression or activity of
CC the fb41a receptor protein, such as regulation of steroid hormone,
CC epinephrine release, gastrointestinal, reproductive, immune, endocrine,
CC musculoskeletal, visceral innervation, neuroendocrine, cognitive, motor
CC coordination, memory, sensory modulation, sensory or motor integration,
CC dopaminergic function, appetite, sensory transmission, olfaction,
CC sympathetic innervation, cardiovascular, respiratory and electrolyte
CC balance disorders, hypertension, diabetes, asthma and migraine. The
CC present sequence represents the amino acid sequence of the human
CC G-protein coupled receptor fb41a.
XX
SQ Sequence 389 AA;

Query Match 99.0%; Score 2035; DB 24; Length 389;

Best Local Similarity 100.0%; Pred. No. 7.3e-225;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 MGFMDNATWTSTFSLVLPNGAHATSPFFNFSDYDMPDDEDESDVNSRTFFFAKIV 64
|||||
DB 1 MGFMDNATWTSTFSLVLPNGAHATSPFFNFSDYDMPDDEDESDVNSRTFFFAKIV 60
|||||
QY 65 IGMALVGIMLVCGIGNFIFIAALVRYKKLNLIANLAIISDFLVAIVCCPFENDYV 124
|||||
DB 61 IGMALVGIMLVCGIGNFIFIAALVRYKKLNLIANLAIISDFLVAIVCCPFENDYV 120
|||||
QY 125 VROLSWEHGHVLTCTSVNYLRTVSLYVSTNALLAIAIDRYLAIYVHPLRPMKQCTATGLIA 184
|||||
DB 121 VROLSWEHGHVLTCTSVNYLRTVSLYVSTNALLAIAIDRYLAIYVHPLRPMKQCTATGLIA 180
|||||
QY 185 LVMTVSTLIAIPSAFTTETVLVIVSQEKIFGQIWPVQOQLYKSYFLFIFGIEFVGP 244
|||||
DB 181 LVMTVSTLIAIPSAFTTETVLVIVSQEKIFGQIWPVQOQLYKSYFLFIFGIEFVGP 240
|||||
QY 245 VVTMTLCYARISRELWFKAYPGFQTEQIRKRLCRRTVLVLMCILTAYVLCWAPFYGFT 304
|||||
DB 241 VVTMTLCYARISRELWFKAYPGFQTEQIRKRLCRRTVLVLMCILTAYVLCWAPFYGFT 300
|||||
QY 305 IVRDFFTVFKKHYLTAFYIVCEIAMSNSMTLTCFVTVKNDTVKYFKKIMLHWKAS 364
|||||
DB 301 IVRDFFTVFKKHYLTAFYIVCEIAMSNSMTLTCFVTVKNDTVKYFKKIMLHWKAS 360
|||||
QY 365 YNGKSSADLDLKTIGMPATEVDCIRLK 393
|||||
DB 361 YNGKSSADLDLKTIGMPATEVDCIRLK 389
RESULT 12
ABP81752
ID ABP81752 standard; Protein; 389 AA.
XX
AC ABP81752;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human G protein-coupled receptor hFB41A protein SEQ ID NO:678.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US50107.
XX
PR 19-DEC-2000; 2000US-257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
PI Burmer GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
DR N-PSDB; AB242597.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating

PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
PS Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (1) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, pain, psoriasis, host
CC disease, Parkinson's disease, multiple sclerosis, graft versus host
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX
XX

Sequence 389 AA;

Query Match 99.0%; Score 2035; DB 24; Length 389;
Best Local Similarity 100.0%; Pred. No. 7.3e-225;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MGFMDNATNTSTFSLVLPNGAHATSPFPNFSYSDYDMPDDEDEVTNSRTFFAAKIV 64
DB 1 MGFMDNATNTSTFSLVLPNGAHATSPFPNFSYSDYDMPDDEDEVTNSRTFFAAKIV 60
QY 65 IGMALVIGMLVCGIGNFIFIAALVRYKKLNLTNLLIANLAISDFLVAIVCCPFEMDYV 124
DB 61 IGMALVIGMLVCGIGNFIFIAALVRYKKLNLTNLLIANLAISDFLVAIVCCPFEMDYV 120
QY 125 VRQLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA 184
DB 121 VRQLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLPRMKCOTATGLIA 180
QY 185 LVWTVSILIAIPSAFYPTETVLVIVKSOEIKFCQIWPVDQOLYKSYFLFIEFVGP 244
DB 181 LVWTVSILIAIPSAFYPTETVLVIVKSOEIKFCQIWPVDQOLYKSYFLFIEFVGP 240
QY 245 VVTMLCYARISRELKFAVPGFOTQIRKLRCKRTVLVLMCILYAVLCHAPFYGYFT 304
DB 241 VVTMLCYARISRELKFAVPGFOTQIRKLRCKRTVLVLMCILYAVLCHAPFYGYFT 300
QY 305 IVRDFFPTVFKKHLYTAFYIVECIAHNSMINTLCFTVTKNDTVYFKKIMLLHWKAS 364
DB 301 IVRDFFPTVFKKHLYTAFYIVECIAHNSMINTLCFTVTKNDTVYFKKIMLLHWKAS 360
QY 365 YNGKSSADLDLKTIGMPATEYDCIRLK 393
DB 361 YNGKSSADLDLKTIGMPATEYDCIRLK 389

RESULT 13

ABB76184
ID ABB76184 standard; Protein: 382 AA.

XX

AC ABB76184;

XX

DT 05-AUG-2002 (first entry)

XX Human G-protein coupled receptor AXOR52.

XX
XX AXOR52; human; G-protein coupled receptor; receptor; viroclide;
XX anti-HIV; analgesic; cytostatic; antidiabetic; osteopathic;
XX antiparkinsonian; cardiac; antiulcer; antiasthmatic; antiallergic;
XX tranquilizer; antidepressant; hypotensive; hypertensive;
XX gene therapy; vaccine.

OS Homo sapiens.

XX GR2368065-A.

XX 24-APR-2002.

XX 09-JUL-2001; 2001GB-0016714.

XX 10-JUL-2000; 2000US-0612772.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Elshourbagy N, Shabon U, Michalovich D, Gattu M, Duckworth M;

XX WPI; 2002-419117/45.

XX N-PSDB; ABL57089.

XX New human AXOR52 receptor polypeptide, useful for treatment and
XX diagnosis of e.g. viral infections, also related nucleic acid,
XX antibodies and modulators -

XX Claim 1; Page 30-31; 35pp; English.

XX The present sequence is the protein sequence for human AXOR52, a
XX novel NPX-like G-protein coupled receptor. The invention provides
XX AXOR52 polypeptides and polynucleotides (see ABL57089), expression
XX vectors, host cells, processes for producing the host cells and
XX polypeptides, and antibodies immunospecific for the AXOR52
XX polypeptide. The polypeptides and polynucleotides may be useful
XX for treatment of bacterial, fungal, protozoan and viral infections
XX (particularly HIV-1 or HIV-2), pain, cancer, diabetes, obesity,

XX anorexia, bulimia, asthma, Parkinson's disease, acute heart
XX failure, hypotension, hypertension, urinary retention,
XX osteoporosis, angina pectoris, myocardial infarction, stroke,
XX ulcers, asthma, allergy, benign prostatic hypertrophy, migraine,
XX vomiting, psychotic and neurological disorders including anxiety,
XX schizophrenia, manic depression, delirium, dementia, and severe
XX mental retardation, and dyskinesias such as Huntington's disease
XX and Gilles de la Tourette's syndrome. They are also useful for
XX identifying agonists and antagonists, in diagnostic assays for
XX detecting diseases associated with inappropriate AXOR52 activity or
XX levels, and in vaccines.

XX Sequence 382 AA;

Query Match 93.6%; Score 1924; DB 23; Length 382;

Best Local Similarity 100.0%; Pred. No. 4.1e-212;

Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METMGFMDDNATNTSTFSLVLPNGAHATSPFPNFSYSDYDMPDDEDEVTNSRTFFA 60
DB 1 METMGFMDDNATNTSTFSLVLPNGAHATSPFPNFSYSDYDMPDDEDEVTNSRTFFA 60
QY 61 AKIVIGMALVIGMLVCGIGNFIFIAALVRYKKLNLTNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVIGMLVCGIGNFIFIAALVRYKKLNLTNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYYVVRQLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLPRMKCOTAT 180
DB 121 DYYVVRQLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLPRMKCOTAT 180
QY 181 GLIALVWTVSILIAIPSAFYPTETVLVIVKSOEIKFCQIWPVDQOLYKSYFLFIEGIE 240
DB 181 GLIALVWTVSILIAIPSAFYPTETVLVIVKSOEIKFCQIWPVDQOLYKSYFLFIEGIE 240

Db 181 GLIALVMTYSILIAIPSAVFTTETVLVIVKSOEKIFCGQWPDQOLYKYSFELFPGIE 240
 QY 241 FVGPPVMTLCVARIISRELWFAVPGFQEQIRKRLRCRKTVLVLMCILTATVLCWAPF 300
 Db 241 FVGPPVMTLCVARIISRELWFAVPGFQEQIRKRLRCRKTVLVLMCILTATVLCWAPF 300
 QY 301 YGFTIVRDFPFTVFKKHYLTAFAIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
 Db 301 YGFTIVRDFPFTVFKKHYLTAFAIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
 QY 361 WKASYNG 367
 Db 361 WKASYNG 367

RESULT 14
 ABG94403
 ID ABG94403 standard; Protein; 393 AA.
 XX AC ABG94403;
 XX DT 27-NOV-2002 (first entry)
 XX DE Rat GPCR protein rZAQ1.
 XX KW G-protein coupled receptor; GPCR; 2AQ; human; 2AQ; 2AQ; rat; 2AQ1;
 KW rZAQ1; rZAQ2; mouse; I5E receptor; m15E; GPR73; Bv8 protein; M15;
 KW digestive disorder; central nervous system disorder; CNS; diarrhoea;
 KW bowel inflammation; constipation; food absorption disorder; nootropic;
 KW Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;
 KW anti-inflammatory; antidiarrhoeic; neuroleptic; neuroprotective;
 XX OS Rattus sp.
 XX PN W0200262944-A2.
 XX PD 15-AUG-2002.
 XX PF 01-FEB-2002; 2002WO-JP00852.
 XX PR 02-FEB-2001; 2001JP-0026820.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
 PI Binuma S;
 XX DR WPI; 2002-627537/67.
 XX N-PSDB; ABS71123.
 XX Screening of compounds modifying the binding of G-protein coupled
 PT receptor protein 2AQ and related proteins to their ligands for use in
 PT treatment and diagnosis of digestive disorders
 XX Claim 1; Page 176-178; 197pp; Japanese.

The present invention relates to a screening method for compounds
 for their ability to modify the binding of G-protein coupled receptor
 (GPCR) protein 2AQ and related proteins (human 2AQ, human 2AQ1,
 rat 2AQ1 (rZAQ1), rZAQ2, human and mouse I5E (m15E) receptor, and
 mouse GPR73) to their ligands (the mature form of human, mouse or rat
 Bv8 protein). The receptor protein and ligand are contacted in the
 presence or absence of the test compound. The compounds are useful
 in a drug composition for the treatment, and prevention of digestive
 and central nervous system (CNS) disorders, including bowel
 inflammation, diarrhoea, constipation, food absorption disorders,
 Alzheimer's disease, Parkinson's disease and schizophrenia.
 The present sequence represents a GPCR or related protein.

Sequence 393 AA;
 Query Match 86.0%; Score 1767; DB 23; Length 393;

Best Local Similarity 84.0%; Pred. No. 4.8e-194;
 Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 METTWGMDNATNTSFLSVLPNGAHATSFNFNSYSDYDMPLEDEEDVTNSRTFFA 60
 Db 1 METTVGTLGENTTNTDFFSARDGSGAETSPLPFTFSYGDYDMPSEDEEDVTNSRTFFA 60
 QY 61 AKIVIGMALVIGMLVCGIGNFIFIAALVRYKRLNLLIANLAISDFLVAIVCCPFEM 120
 Db 61 AKIVIGMALVIGMLVCGIGNFIFITALARYKRLNLLIANLAISDFLVAIVCCPFEM 120
 QY 121 DYYVYRQLSWEGHVLCTSVNYLRTVSLYSTNALLAIAIDRYLAIYHPLRPMKQATAT 180
 Db 121 DYYVYRQLSWEGHVLCTSVNYLRTVSLYSTNALLAIAIDRYLAIYHPLRPMKQATAA 180
 QY 181 GLIALVMTYSILIAIPSAVFTTETVLVIVKSOEKIFCGQWPDQOLYKYSFELFPGIE 240
 Db 181 GLIFLWMSVSLIAIPAAFTTETVLVIVSQQEIKFCGQWPDQOLYKYSFELFPGIE 240
 QY 241 FVGPPVMTLCVARIISRELWFAVPGFQEQIRKRLRCRKTVLVLMCILTATVLCWAPF 300
 Db 241 FVGPPVMTLCVARIISRELWFAVPGFQEQIRKRLRCRKTVLVLMCILTATVLCWAPF 300
 QY 301 YGFTIVRDFPFTVFKKHYLTAFAIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
 Db 301 YGFTIVRDFPFTVFKKHYLTAFAIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
 QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
 Db 361 WRASPSGSKASADLDLRTTGIPATEEVDICRLK 393

RESULT 15
 ABG99158
 ID ABG99158 standard; Protein; 393 AA.
 XX AC ABG99158;
 XX DT 15-NOV-2002 (first entry)
 XX DE Rat rZAQ1 protein.
 XX KW Rat; physiological; G protein-coupled receptor; 2AQ; antidiarrhoeic;
 KW laxative; anti-inflammatory; digestive disease; diarrhoea; constipation;
 KW colitis; gene therapy; rZAQ1.
 XX OS Rattus sp.
 XX PN W0200262996-A1.
 XX PD 15-AUG-2002.
 XX PF 01-FEB-2002; 2002WO-JP00837.
 XX PR 02-FEB-2001; 2001JP-0026798.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Ohtaki T, Masuda Y, Takatsu Y;
 XX WPI; 2002-627554/67.
 XX N-PSDB; ABQ79092.
 XX Physiologically-active brain-originated G protein-coupled receptor
 PT peptide 2AQ and encoding DNA, useful for developing drugs to treat
 PT digestive diseases e.g. diarrhoea, constipation and colitis, including
 PT gene therapy
 XX Claim 16; Page 161-163; 184pp; Japanese.
 XX The invention relates to a novel physiologically-active brain-originated
 CC G protein-coupled receptor peptide designated 2AQ. The proteins of the
 CC invention have antidiarrhoeic, laxative, and anti-inflammatory activity.

CC The DNA and encoded protein are useful for developing drugs for the
CC treatment of diseases of the digestive organs e.g. diarrhoea,
CC constipation and colitis. The polynucleotides may have a use in gene
CC therapy. The sequence represents a rat 2A0 (r2A01) protein of the
CC invention.

xx

SQ Sequence 393 AA;

```
Query Match      86.0%; Score 1767; DB 23; Length 393;
Best Local Similarity 84.0%; Pred. No. 4.8e-194;
Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 METTMGFMDNATNTSTSLVLPNGAHATSPFPNFYSYSDYDMPDDEDEDTNSRTFFA 60
   ||||| : : ||| : : : ||| : ||| ||||| |||||
Db 1 METTVGLGENTNTTDFESARDGSGATSPLPFTFSYGYDMPDSEEDVTNSRTFFA 60
   ||||| : : ||| : : : ||| : ||| ||||| |||||

QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AKIVIGMALVGMVCGIGNFIFITALARYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 DXYVVRQLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 DXYVVRQLSWEHGHVLCASVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOATA 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSOEKIFCGIWPVDQOQYKSYFLFIFGIE 240
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 181 GLIFLWVSILIAIPAAYFTTETVLVIVESQEKIFCGIWPVDQOQFYRSYFLLVFGL 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 FVGPTVTHLTCYARISRELWFKAVPGFQTEQIRKRLRCRRKTVLVMCILTAIVLCAWPF 300
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 241 FVGPIAMTLCYARVSRELWFKAVPGFQTEQIRRLRCRRRTVLGLVCVLSAYVLCWAPF 300
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 301 YGFTIYRDFPPTVVKKHVLTAFYIVECIAMNSMINTLCFVTVKNDVVKYFKKIMLLH 360
   ||||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 301 YGFTIYRDFPSPVFKKHVLTAFYIVVECIAMNSMINTLCFVTVRNNTSKYLKRLRLQ 360
   ||||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 361 WKASYNGKSSADLDLKTIGMPATEEVDCIRLK 393
   ||||| : ||||| : ||||| : ||||| : |||||
Db 361 WRASPSGSKASADLDLRTTGIPATEEVDCIRLK 393
   ||||| : ||||| : ||||| : ||||| : |||||
```

Search completed: October 7, 2003, 09:51:48
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 09:49:27 ; Search time 19 Seconds
(without alignments)
1989.173 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTMGFMDNDATNTSTSLF.....LDLKTGMPTAEVDCIRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 405 | 19.7 | 449 | 2 A41738 | neuropeptide Y rec |
| 2 | 387.5 | 18.9 | 381 | 2 I39187 | neuropeptide Y/pep |
| 3 | 387.5 | 18.9 | 519 | 2 S17793 | tachykinin receptio |
| 4 | 367.5 | 17.9 | 370 | 1 I52315 | G protein-coupled |
| 5 | 363 | 17.7 | 384 | 2 S20303 | neurokinin 1 recep |
| 6 | 362.5 | 17.6 | 407 | 2 A34357 | neurokinin 1 recep |
| 7 | 360.5 | 17.5 | 407 | 2 S20304 | neurokinin 1 recep |
| 8 | 356.5 | 17.3 | 407 | 1 J01274 | neurokinin 1 recep |
| 9 | 354.5 | 17.3 | 407 | 2 S23510 | neurokinin 1 recep |
| 10 | 354 | 17.2 | 384 | 2 I57957 | neurokinin 2 recep |
| 11 | 354 | 17.2 | 398 | 1 J01059 | neurokinin 2 recep |
| 12 | 347 | 16.9 | 384 | 1 S00516 | neurokinin 2 recep |
| 13 | 340 | 16.5 | 402 | 2 I56595 | neurokinin 2 recep |
| 14 | 338 | 16.4 | 390 | 2 A36737 | neurokinin 2 recep |
| 15 | 334.5 | 16.3 | 391 | 2 A41795 | somatostatin recep |
| 16 | 334.5 | 16.3 | 391 | 2 C41795 | somatostatin recep |
| 17 | 334.5 | 16.3 | 391 | 2 A39297 | somatostatin recep |
| 18 | 332.5 | 16.2 | 465 | 1 J01517 | neurokinin 3 recep |
| 19 | 328.5 | 16.0 | 384 | 2 A47249 | brain-specific som |
| 20 | 327 | 15.9 | 504 | 2 A41783 | tachykinin recepto |
| 21 | 325.5 | 15.8 | 384 | 2 J04629 | somatostatin recep |
| 22 | 324.5 | 15.8 | 452 | 2 A34916 | neurokinin 3 recep |
| 23 | 321.5 | 15.6 | 349 | 2 I59336 | galanin receptor 1 |
| 24 | 320 | 15.6 | 375 | 2 S63685 | neuropeptide Y rec |
| 25 | 320 | 15.6 | 385 | 2 S55524 | neurokinin 3 recep |
| 26 | 319 | 15.5 | 440 | 2 A44081 | kappa-type opioda |
| 27 | 314 | 15.3 | 357 | 2 J07339 | probable allatosta |
| 28 | 309.5 | 15.1 | 423 | 2 B40470 | glucocorticoid-ind |
| 29 | 309 | 15.0 | 394 | 2 J07209 | galanin receptor - |

ALIGNMENTS

RESULT 1

A41738

neuropeptide Y receptor - fruit fly (Drosophila melanogaster)

N:Alternate names: G protein-coupled receptor PR4

C:Species: Drosophila melanogaster

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Apr-2000

C:Accession: A41738

R:Li, X.-J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-12, 1992

A:Title: Cloning, functional expression, and developmental regulation of a neuropep

A:Reference number: A41738; MUID:92112730; PMID:1370455

A:Accession: A41738

A:Molecule type: mRNA

A:Residues: 1-449 <LIA>

A:Cross-references: GB:M81490; NID:gl57996; PIDN:AAA28727.1; PID:gl57997

C:Genetics:

A:Gene: FlyBase:Nepyr

A:Cross-references: FlyBase:FBgn0004842

C:Superfamily: neurokinin 1 receptor

C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

| | | | | | | | |
|-----------------------|-------|---|----------|------------|------|--------|------|
| Query Match | 19.7% | Score | 405; | DB | 2; | Length | 449; |
| Best Local Similarity | 30.0% | Pred. No. | 4.3e-27; | | | | |
| Matches | 115; | Conservative | 70; | Mismatches | 128; | Indels | 70; |
| Gaps | 15; | | | | | | |
| Qy | 9 | DDNATN---TSTFSLVNLPHGARATSPFNFSYSDYDMLDEDEDVTNSRTFFAAKIVI | 65 | | | | |
| Db | 41 | DOEGSNYGYGTTTSLGLOFETYNITVM--NMFSCDDYDL---LSEDMWSSAYF---KIIIV | 93 | | | | |
| Qy | 66 | GMALVGIMLVCGIGNFFIAALVRYKKRLNLTLLIANLAISDFLVAIVCCP-----FE | 119 | | | | |
| Db | 94 | YMLXIPFIFALNGTGVICIVSTPRRVTVNYFIASLALGILMSFFCEPSSFLFI | 153 | | | | |
| Qy | 120 | MDYVYVROLSEWGHVLCVTSVNTLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKQTA | 179 | | | | |
| Db | 154 | LNY-----WPGGLALCHFNVTSSQAVSLVSAVTLVAISIDRYIALMPLKPRITRYA | 206 | | | | |
| Qy | 180 | TGLIALVWTVSILIAIP-----SAFTTETVLVIVKSOEKIFCCQIWPVDQOOLY | 228 | | | | |
| Db | 207 | TFIIAGVMFIALATALPIPIVGLDIPMSPHWT-----KCEYICHEMPSRSQY | 257 | | | | |
| Qy | 229 | YKSVFLPIFIEFGVPVWTLCVARSRLWFKAVPG-FOTEQIRKRLCRKTKVLVLM | 287 | | | | |
| Db | 258 | Y--YTLSLFALQFVPLGVGLIFTYARITRWAKRPPGEAETNRDQMAKSKRWVQML | 315 | | | | |
| Qy | 288 | CILTAYVLCNAPYFGFTVRD-----FFPTVFVKKHLYLTAFYIVECIANSMSNLT- | 340 | | | | |
| Db | 316 | TVWIVFTCCWLPENILQLLNDDEFAHWDPLPYV-----WFAFWLANSCCNPPII | 367 | | | | |
| Qy | 341 | -CFYVVKNDVYKFKK--IMLLH | 360 | | | | |
| Db | 368 | CYMNNAR-----FRSGFVQLMH | 384 | | | | |

293 ---TAMSSSTWNPITYCCI-ND 310

Db 234 DRYHEQVSAKRKVKVMHVVVCTFAICWLPFHIFLLPYNPDLYLK-KFIQQVYLAIMW 292
QY 330 IAMSNSMINTLCFTYVKNQ 348
Db 293 LAMSSTWNPPIIYCCCL-ND 310

RESULT 9
S23510
neurokinin 1 receptor - guinea pig
N:Alternate names: NK-1 receptor; substance P receptor
C:Species: Cavia porcellus (guinea pig)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 19-May-2000
C:Accession: S23510; S19198
R:Gorbulev, V.; Akhundova, A.; Luzius, H.; Fahrenholz, F.
Biochim. Biophys. Acta 1131, 99-102, 1992
A:Title: Molecular cloning of substance P receptor cDNA from guinea-pig uterus.
A:Reference number: S23510; MUID:92256498; PMID:1374648
A:Accession: S23510
A:Molecule type: mRNA
A:Residues: 1-407 <GOR>
A:Cross-references: EMBL:X64323; NID:q49565; PIDN:CAA45608.1; PID:q49566
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:32-55/Domain: transmembrane #status predicted <TM1>
F:69-89/Domain: transmembrane #status predicted <TM2>
F:117-128/Domain: transmembrane #status predicted <TM3>
F:149-169/Domain: transmembrane #status predicted <TM4>
F:196-217/Domain: transmembrane #status predicted <TM5>
F:250-280/Domain: transmembrane #status predicted <TM6>
F:289-308/Domain: transmembrane #status predicted <TM7>

Query Match 17.3%; Score 354.5; DB 2; Length 407;
Best Local Similarity 24.8%; Pred. No. 8.5e-23;
Matches 79; Conservative 85; Mismatches 134; Indels 21; Gaps 9;

QY 41 DYDMLPED-----EDVNSRTFF--AAKIVIGMALVGLMVG-IGNFTIFIAALVRYK 91
Db 2 DNVLPVSDLPFNISTNTSEPNQVQPAQWQVLAIAATVITVTSVGVNVMIIILAK 61

QY 92 KLRNLTLNLTANLALSFVAIVCCPEMDYVYVQRLSWEGHVLCTSYNLYRVLVSVS 151
Db 62 RMRVTNVLNLTAFASMAAFNTVNVFTYAVHNE--WYGLFCYKPHNFPPAAVFA 119

QY 152 TNALLATAIDRYLAIVHPLRPMKQATGLIALVWTVSILAIAPSAVF-TTEVLVIVK 210
Db 120 IYSTAVAFDRYMAIIHPLQRLSATATKVICVIVWLAULLAFPGGYSTETM----- 174

QY 211 SQEKFQCIQWV-DQQLYKSYFLFIFGIEFVGVPVMTLCYARISRELWFAVPGFOT 269
Db 175 -PGRVCMIEPNSHPDKIYKVKYHICVTLVYFLPLVIGVAYTVWGTLLWASEIPGDS 233

QY 270 EQIRKRLCRKTVLWLCILTAIVLWAPYGGTIVRDFPTVFKKHLTAIFYIVEC 329
Db 234 DRYHEQVSAKRKVKVMHVVVCTFAICWLPFHIFLLPYNPDLYLK-KFTQQVYLAIMW 292

QY 330 IAMSNSMINTLCFTYVKNQ 348
Db 293 LAMSSTWNPPIIYCCCL-ND 310

RESULT 10
157957
neurokinin 2 receptor - hamster
N:Alternate names: neurokinin A receptor; NK-2 receptor; substance K receptor (SKR)
C:Species: Cricetinae gen. sp. (hamster)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-May-2000
C:Accession: I57957
R:Aharony, D.; Little, J.; Thomas, C.; Powell, S.; Berry, D.; Graham, A.
Mol. Pharmacol. 45, 9-19, 1994
A:Title: Isolation and pharmacological characterization of a hamster urinary bladder neu
A:Reference number: 157957; MUID:94134065; PMID:8302285
A:Accession: I57957

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-384 <RES>
A:Cross-references: GB:S68899; NID:q545230; PIDN:AAC60680.1; PID:q545231
C:Superfamily: neurokinin 1 receptor

Query Match 17.2%; Score 354; DB 2; Length 384;
Best Local Similarity 27.4%; Pred. No. 8.8e-23;
Matches 94; Conservative 65; Mismatches 140; Indels 44; Gaps 10;

QY 8 MDDNATNTSTSLSVLNPHGHAHATSPFFNFSTSDYDMPDEDEDVNTSTFFAAKIVL-G 66
Db 1 MCGRAIVTDTNIFSGLESNTGTAF-----SMP-----AWQLALWA 37

QY 67 MALVGLNVLGCGIGNFFIAALVYKRLNLTLLIANLAISDFLVAIVCCPEMDYVYVVR 126
Db 38 TAYLGLVAVTGNATVIMIIIAHERRTVWYFINLALADLCMAAFNATFNFY--AS 95

QY 127 QLSWEGHVLCTSVNYLRTVSVLSTNALLAIDRYLAIVHPLRPMKQATATGLIALV 186
Db 96 HNIWFGRAFCYFQNLFPITAMFVSIYSTAIAADRYMAIVHVPQPLRSAPITKATIAGI 155

QY 187 WTVSILAIPTSAFTTETVLVIVKSEKIFCGQIWPVD---QQLYKSYFLFIFGIEFVG 243
Db 156 WLVALALASQCCFYSTIV-----DQCATKCVVAMPNDNGKMLLL--YHLVVFVLVYFL 208

QY 244 PVTMTLCYARISRELWFAVPGFQTEIRKR-LRCRRKTVLWLCILTAIVLWAPYFG 302
Db 209 PLVYMFVAVSIGLTWKRVPVPHQAGNLRHLHAKKFKYKAVLVLTFAICWLPYHL 268

QY 303 FTIVRDFPPTVYVK---EKHYLFAFYVECIAMNSMINTLCF 342
Db 269 YFILGSGFQDIYVRKFTQQVYLLAFW----LAMSSTWNPPIIY 307

RESULT 11
JQ1059
neurokinin 2 receptor - human
N:Alternate names: neurokinin A receptor; NK-2 receptor; substance K receptor (SKR)
C:Species: Homo sapiens (man)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: JQ1059; JS0575; A23658; A61224
R:Graham, A.; Hopkins, B.; Powell, S.J.; Danks, P.; Briggs, I.
Biochem. Biophys. Res. Commun. 177, 8-16, 1991
A:Title: Isolation and characterization of the human lung NK-2 receptor gene using
A:Reference number: JQ1059; MUID:91254341; PMID:1710456
A:Accession: JQ1059
A:Molecule type: DNA
A:Residues: 1-398 <GRA1>
A:Cross-references: GB:M75105; NID:g189219; PIDN:AAB05897.1; PID:g189222
A:Accession: JS0575
A:Molecule type: mRNA
A:Residues: 1-398 <GRA2>
A:Cross-references: GB:M75105; NID:g189219; PIDN:AAB05897.1; PID:g189222
A:Experimental source: lung
A>Note: 23-Ile and 375 His were also found
R:Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
J. Biol. Chem. 265, 20455-20462, 1990
A:Title: The human neurokinin A (substance K) receptor. Molecular cloning of the ge
A:Reference number: A23658; MUID:91056095; PMID:2173708
A:Accession: A23658
A:Molecule type: DNA
A:Residues: 1-22,'I',24-240,'L',242-398 <GER>
A:Cross-references: GB:M60284; GB:J05680; NID:g189140
A>Note: the authors translated the codon GGA for residue 317 as Glu
R:Kris, R.M.; South, V.; Saltzman, A.; Feider, S.; Ricca, G.A.; Jaye, M.; Huebner, I
Cell Growth Differ. 2, 15-22, 1991
A:Title: Cloning and expression of the human substance K receptor and analysis of i
A:Reference number: A61224; MUID:91175483; PMID:1848773
A:Accession: A61224
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-22,'I',24-293,'F',294-374,'H',376-398 <KRI>

K; SASAI, I.; NAKAMISHI, S.
Biochem. Biophys. Res. Commun. 165: 695-702, 1989.

A:Title: Molecular characterization of rat substance K receptor and its mRNAs.
A:Reference number: A36737; MUID:90088481; PMID:2480781

A:Accession: A36737

A:Molecule type: mRNA

A:Residues: 1-390 <SAS>

A:Cross-references: GB:M31838; NID:g206986; PIDN:AAA42150.1; PID:g206987

C:Superfamily: neurokinin 1 receptor

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 16.4%; Score 338; DB 2; Length 390;

Best Local Similarity 28.2%; Pred. No. 2.1e-21;

Matches 80; Conservative 62; Mismatches 118; Indels 24; Gaps 7;

QY 68 ALVGIMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVVRQ 127

DB 39 AYALVAVAVGNTVNTWILAHARTVNTFIILALADLCHAAFNATFNFIY--ASH 96

QY 128 LSWEHGHVLCSTVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLRPRMKQATGGLIALVM 187

DB 97 NIWYGFACFCYFONLFPITAMFVSIYSMTAIAADRYMAIVHPFPRLSAPSTRKAIAGIW 156

QY 188 TVSILTAIPSAFTTETVLVIVKSKQEKIFCGQIWPVDO-----QLYKSKSEFLFIFGIEFV 242

DB 157 LVALALASQCFYSTIV-----DEGATKCVVAMPNDNGKMLLLYHLVVFVLIYEL--- 208

QY 243 GPVVTWTLVCIARISRELWFKAVPGFQTEQIRKRLCRRTVLVLMCILTAIVYLCHWAPFY 301

DB 209 -PLLVNFGAYSVGLTLWKRVRPHQAGNLRHLQAKKFKYKAMVLVLTFAICMLPHY 267

QY 302 GFTIVRDFPTFVVK---EKHYLTAFYIVECIAMSNMINTLCF 342

DB 268 LYPILGTQEDIIYHKFIQQVYLALFW----LAMSMTYNPIIY 307

RESULT 15

A41795

somatostatin receptor 1 - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999

C:Accession: A41795

C:Amada, F.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992

A:Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors

A:Reference number: A41795; MUID:92108031; PMID:1346068

A:Accession: A41795

A:Molecule type: DNA

A:Residues: 1-391 <YAM>

A:Cross-references: GB:M81829; NID:g307433; PIDN:AAA58247.1; PID:g307434

A:Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIIP:74768)

C:Genetics:

A:Gene: GDB:SSTR1

A:Cross-references: GDB:134185; OMIM:182451

A:Map position: 14q13-14q13

A:Introns: #status absent

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phd

F:58-84/Domain: transmembrane #status predicted <TM1>

F:95-120/Domain: transmembrane #status predicted <TM2>

F:132-153/Domain: transmembrane #status predicted <TM3>

F:173-195/Domain: transmembrane #status predicted <TM4>

F:220-250/Domain: transmembrane #status predicted <TM5>

F:269-296/Domain: transmembrane #status predicted <TM6>

F:302-326/Domain: transmembrane #status predicted <TM7>

F:4.44.48.381/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:130-208/disulfide bonds: #status predicted

F:172/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predicted

F:265/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted

F:339/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match

Best Local Similarity 16.3%; Score 334.5; DB 2; Length 391;

Matches 85; Conservative 68; Mismatches 128; Indels 21; Gaps 8;

Search completed: October 7, 2003, 09:52:13

Job time: 21 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:47:46 ; Search time 15 seconds
(without alignments)
1232.100 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTMGFMDNATNTSTSL.....LDLTIGMPATEVDCIRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Length | DB ID | Description |
|------------|-------|---------|--------|---------------|---------------------|
| 1 | 416.5 | 20.3 | 385 | 1 NY2R_CHICK | Q9ddn6 gallus gall |
| 2 | 405 | 19.7 | 449 | 1 NYR_DRONE | P25931 drosophila |
| 3 | 393.5 | 19.1 | 382 | 1 NY2R_PIG | O02836 sus scrofa |
| 4 | 391 | 19.0 | 384 | 1 NY2R_BOVIN | P79113 bos taurus |
| 5 | 390.5 | 19.0 | 385 | 1 NY2R_MOUSE | P97295 mus musculus |
| 6 | 387.5 | 18.9 | 381 | 1 NY2R_HUMAN | P49146 homo sapien |
| 7 | 387.5 | 18.9 | 519 | 1 TLR2_DRONE | P30975 drosophila |
| 8 | 384.5 | 18.7 | 381 | 1 NY2R_MACACO | Q9gk74 macaca mula |
| 9 | 379 | 18.4 | 381 | 1 NY2R_CAYPO | P49683 homo sapien |
| 10 | 370 | 18.0 | 370 | 1 GP10_HUMAN | Q64121 rattus norv |
| 11 | 367.5 | 17.9 | 370 | 1 NK2R_MOUSE | P30549 mus musculus |
| 12 | 363 | 17.7 | 384 | 1 NK1R_RAT | P14600 rattus norv |
| 13 | 362.5 | 17.6 | 407 | 1 NK1R_RAT | P30548 mus musculus |
| 14 | 360.5 | 17.5 | 407 | 1 NK1R_MOUSE | P79218 oryctolagus |
| 15 | 358 | 17.4 | 384 | 1 NK2R_RABIT | P25103 homo sapien |
| 16 | 356.5 | 17.3 | 407 | 1 NK1R_HUMAN | P30547 cavia porce |
| 17 | 354.5 | 17.3 | 407 | 1 NK1R_CAYPO | P51144 mesocricetu |
| 18 | 354 | 17.2 | 384 | 1 NK2R_MESCAT | P21452 homo sapien |
| 19 | 354 | 17.2 | 398 | 1 NK2R_HUMAN | O43613 homo sapien |
| 20 | 351 | 17.1 | 425 | 1 OX1R_HUMAN | P05363 bos taurus |
| 21 | 347 | 16.9 | 384 | 1 NK2R_BOVIN | P56718 rattus norv |
| 22 | 347 | 16.9 | 416 | 1 OX1R_RAT | O43614 homo sapien |
| 23 | 345 | 16.8 | 444 | 1 OX2R_HUMAN | P58308 mus musculus |
| 24 | 344 | 16.7 | 460 | 1 OX2R_MOUSE | Q87up7 canis fami |
| 25 | 343.5 | 16.7 | 444 | 1 OX2R_CANFA | P36719 rattus norv |
| 26 | 343 | 16.7 | 460 | 1 OX2R_RAT | Q84077 cavia porce |
| 27 | 340 | 16.5 | 402 | 1 NK2R_CAYPO | Q98982 rana catesb |
| 28 | 339.5 | 16.5 | 408 | 1 NK1R_RANCA | P16610 rattus norv |
| 29 | 338 | 16.4 | 390 | 1 NK2R_RAT | Q62805 rattus norv |
| 30 | 337 | 16.4 | 346 | 1 GALR_RAT | P36479 mus musculus |
| 31 | 336 | 16.4 | 348 | 1 GALR_MOUSE | Q9ttq9 canis fami |
| 32 | 335 | 16.3 | 422 | 1 GP72_CANFA | P30974 drosophila |
| 33 | 335 | 16.3 | 504 | 1 TLR1_DRONE | |

RESULT 1
NY2R_CHICK
ID NY2R_CHICK STANDARD; PRT; 385 AA.
AC Q9DDN6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).
GN NPY2R.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP MEDLINE=20532533; PubMed=11078884;
RA Salanek E., Holmberg S.K., Berglund M.M., Boswell T., Larhammar D.;
RT Chicken neuropeptide Y receptor Y2: structural and pharmacological
RT differences to mammalian Y2.*;
RL FEBS Lett. 484:229-234(2000).
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: TACHIKININS RECEPTORS.

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or send an email to license@sib-sib.ch).

EMBL: AF309091; AAC37898.1; -
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PRINTS; PRO0237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1;
DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 53 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 54 76 1 (POTENTIAL).
FT DOMAIN 77 86 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 87 108 2 (POTENTIAL).
FT DOMAIN 109 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 150 3 (POTENTIAL).
FT DOMAIN 151 170 4 (POTENTIAL).
FT DOMAIN 171 191 4 (POTENTIAL).
FT DOMAIN 192 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 244 5 (POTENTIAL).
FT DOMAIN 245 272 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 273 295 6 (POTENTIAL).
FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 309 332 7 (POTENTIAL).

ALIGNMENTS

| | | | | | | |
|----|-------|------|-----|---|------------|---------------------|
| 34 | 334.5 | 16.3 | 391 | 1 | SSR1_HUMAN | P30872 homo sapien |
| 35 | 334.5 | 16.3 | 391 | 1 | SSR1_MOUSE | P30873 mus musculus |
| 36 | 334.5 | 16.3 | 391 | 1 | SSR1_RAT | P28646 rattus norv |
| 37 | 332.5 | 16.2 | 465 | 1 | NK3R_HUMAN | P29371 homo sapien |
| 38 | 328.5 | 16.0 | 384 | 1 | SSR4_RAT | P30937 rattus norv |
| 39 | 327.5 | 15.9 | 467 | 1 | NK3R_RABIT | O97512 oryctolagus |
| 40 | 327 | 15.9 | 371 | 1 | NY6R_MOUSE | Q61212 mus musculus |
| 41 | 327 | 15.9 | 452 | 1 | NK3R_MOUSE | P47937 mus musculus |
| 42 | 325.5 | 15.8 | 384 | 1 | SSR4_MOUSE | P49660 mus musculus |
| 43 | 325.5 | 15.8 | 423 | 1 | GP72_HUMAN | O99ym4 homo sapien |
| 44 | 324.5 | 15.8 | 452 | 1 | NK3R_RAT | P16177 rattus norv |
| 45 | 321.5 | 15.6 | 349 | 1 | GALR_HUMAN | P47211 homo sapien |


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FT DOMAIN 333 385 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 127 207 BY SIMILARITY.
FT LIPID 346 346 PALMITATE (POTENTIAL).
SQ SEQUENCE 385 AA; 43509 MW; 60A09B314E665B62 CRC64;

Best Match
Query Local Similarity 30.3%; Score 416.5; DB 1; Length 385;
Matches 93; Conservative 75; Mismatches 132; Indels 7; Gaps 4;

QY 43 DMPLDEDEVTNSRTFFRAAKIVGIMVIMVCGIGNFIFIAALVRYKKRLNLTNLLIA 102
DB 35 ELALDPKPKLSTLLVEVOIILIPAYGSIILLVIGNSLVHVIKPKSMRTVTFEIA 94
QY 103 NLAISDFVAIVCCPFEMDYVVVROLSEHGHLVCTSVNLTSTVSLVSTNALLAIDR 162
DB 95 NLAVALDLVNTLCLEFTLVYLLGE--NKLGPVLCHLVPAQALAVHVTVLVIALDR 152
QY 163 YLAIVHPLPRMKCOTATGLIALVWTSILIAIPSAFTTETVLVIVKSEKIFCGIWP 222
DB 153 HRCIVVHLESKISKISFLIGVAVASALLASPLAFREYSLEIIPDFKIVVCSKWP 212
QY 223 VDQQLYYAS-YLFTEGIEFVCPVVTMTLCYARISRELWFKAVPGFQEQIKRLCRK 281
DB 213 GEGQNYGTIYSVMLLIQYVLPALAIISYATRIWTKLNHVSOGAGNDHYHHR---RQK 269
QY 282 TVLVLMCILTAVLVCAWPFYGTIVRDFPTVFVKEKHYLTAFYIVCEIAMSNSMINTLC 341
DB 270 TTKMLVCVVVFAVSWLPHAFQVLDSDSQV-LDLKEYKLIYTVFHVIMCSTFANPLL 328
QY 342 FVTYVND 348
DB 329 YGWMANN 335
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RESULT 2
NYR_DROME STANDARD; PRT; 449 AA.
AC P25931;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Neuropeptide Y receptor (NPY-R) (NP4 receptor).
GN NEPYR.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=92112730; PubMed=1370455;
RX Li X.-J., Wu Y.-N., North R.A., Forte M.;
RA "Cloning, functional expression, and developmental regulation of a
RT neuropeptide Y receptor from Drosophila melanogaster.";
RL J. Biol. Chem. 267:9-12(1992).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DEVELOPMENTAL STAGE: AT LOW LEVELS DURING EARLY EMBRYONIC STAGES,
CC ITS EXPRESSION INCREASES LATER AND REACHES THE HIGHEST LEVEL
CC DURING LATE STAGES OF EMBRYOGENESIS. SUBSEQUENTLY, PRA LEVELS ARE
CC REDUCED DURING LARVAL STAGES AND INCREASE DURING PUPAL STAGES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININ RECEPTORS.
-----
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CC
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DR EMBL; M81490; AAA28727.1; -.
DR PIR; A41738; A41738.
DR FlyBase; FBgn004842; Npyr.
DR InterPro; IPR000276; GPCR_Rhodops.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 85 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 86 111 1 (POTENTIAL).
FT DOMAIN 112 120 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 121 145 2 (POTENTIAL).
FT DOMAIN 146 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 187 3 (POTENTIAL).
FT DOMAIN 188 203 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 204 232 4 (POTENTIAL).
FT DOMAIN 233 256 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 257 282 5 (POTENTIAL).
FT DOMAIN 283 309 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 310 330 6 (POTENTIAL).
FT DOMAIN 331 347 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 348 372 7 (POTENTIAL).
FT DOMAIN 373 449 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 449 AA; 51885 MW; IADB32EPD50146G3 CRC64;

Query Match 19.7%; Score 405; DB 1; Length 449;
Best Local Similarity 30.0%; Pred. No. 8.7e-22;
Matches 115; Conservative 70; Mismatches 128; Indels 70; Gaps 15;

QY 9 DDNATN---TSTFSLVNLPHGAHATSPFNFSYSDYDMLDDEDEVTNSRTFAAKIVI 65
DB 41 DDEGSNYGSGTTLTSLGLQFETYNITVM-MNFCDDYDL---LSEDMWSAYF---KIV 93
QY 66 GMALVGLMVGCGIGNFIFIAALVRYKKRLNLTNLLIAISDFLVAIVCCP-----FE 119
DB 94 YMLYIPFIPALIGNTCYIVYVSTPRMRTVNYFIASLADILNGFFCEPSSFSILFI 153
QY 120 MDYVYVQLSWEHGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLPRMKQTA 179
DB 154 LNY-----WPFGLALCHFYNSQAVSVLSVLTVAISIDRYIAIMPLKPRITRYA 206
QY 180 TGLIALVTVSILTAIP-----SAFTTETVLVIVKSEKIFCGIWPVDQQLY 228
DB 207 TFIAGVWFIALATALPIPIVSGLDIPMSPHT-----KCEKYICRMWPSRSQY 257
QY 229 YKSYELFIFIGIEFVGPVVTMTLCYARISRELWFKAVPG-FQTDQIRKRLCRRTVLVLM 287
DB 258 Y--YTLSEFALQFVPLGLVLIFFYARITIRWAKRPPGEAETNRDQRMARSKRMKWL 315
QY 288 CILRAYVLCAWPFYGTIVRD-----FFPVPVFKKHLYTAFYIVCEIAMSNSMINTL- 340
DB 316 TVVITCCMLPFLNLLQLLNDEEFAHMDPLPYV-----WFAFWLHLSHCCYNPII 367
QY 341 -CFVTYVNDTVKYFKK--IMLLH 360
DB 368 YCYNNAR-----FRSGFVQLMH 384

RESULT 3
NY2R_PIG STANDARD; PRT; 382 AA.
AC O02836; O2ST11;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-v2 receptor).
GN NPY2R.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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FT DOMAIN 191 217 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 218 243 5 (POTENTIAL).
FT DOMAIN 244 271 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 272 294 6 (POTENTIAL).
FT DOMAIN 295 307 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 308 331 7 (POTENTIAL).
FT DOMAIN 332 384 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 126 206 BY SIMILARITY.
FT LIPID 345 PALMITATE (POTENTIAL).
SQ SEQUENCE 384 AA; 42943 MW; 468D19CBA8F29681 CRC64;

Query Match 19.0%; Score 391; DB 1; Length 384;
Best Local Similarity 28.6%; Pred. No. 7.4e-21;
Matches 100; Conservative 77; Mismatches 159; Indels 14; Gaps 5;

QY 5 MGFMDNATNTSTFSLVNLPHGAHATSFPPNFSDYDMPLEDEDEDVNSRTFAKIV 64
DB 3 MGLPAGAEADENQTVEMKVDQFGPGHHTLP-----GELAPDSEPELIDSTKLEIYQV 55
QY 65 IGMALVGLMVGIGNFIIFIAALVRYKRLNLTLLIANLAISDFLVAIVCCPFEMDYV 124
DB 56 LILAYCSIIILGVIGNSLVHVIKFSKRTVNFIFIANLAVADLLVNTLCPLFTLTYL 115
QY 125 VROLSEHGHLVCTSYNLTSLVSVNALLAIAIDRYLAIVHPLRPMKQATGLIA 184
DB 116 MGE--WKMGVPLCHLVPAQGLAVQVSTLTITVIALDRHRCIVYHLESKISKISFLIG 173
QY 185 LVMTYSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQO-LYIKSYELFIKIEFVG 243
DB 174 LAMGVSALLASPLAIFREYSLIEIIPDFEIVACTEKWPGEEKGIYGTYSLSLLILTYL 233
QY 244 PVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRRTKTLVLMCILRAYVLCNAPFYGF 303
DB 234 PLGIISFSTYRIMSKLNHVSFGAHDYHQR---RQNTKMLVCVVVVEAVSNLPLHAF 290
QY 304 TIVRDFPTVFVKEKHYLTAFYIVCEIAMSNSMINTLCFTVVKNDTVKIF 353
DB 291 QLAVDIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLLYGWNNSYKRAF 339

RESULT 5
NY2R_MOUSE STANDARD; PRT; 385 AA.
AC P97295;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).
GN NPY2R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97071731; PubMed=8914576;
RA Nakamura M., Aoki Y., Hirano D.;
RT "Cloning and functional expression of a cDNA encoding a mouse type 2
RT neuropeptide Y receptor.";
RL Biochim. Biophys. Acta 1284:134-137(1996).
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC -----
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CC -----
CC EMBL; D86238; BAA13050.1; --
CC MGD; MGI:108418; NPY2R.
CC GO; GO:0001601; F:peptide YY receptor activity; IDA.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN_RECEPT_FL_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECEPT_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 53 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 54 76 1 (POTENTIAL).
FT DOMAIN 77 86 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 87 108 2 (POTENTIAL).
FT DOMAIN 109 128 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 129 150 3 (POTENTIAL).
FT DOMAIN 151 170 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 218 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 219 244 5 (POTENTIAL).
FT DOMAIN 245 272 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 273 295 6 (POTENTIAL).
FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 309 332 7 (POTENTIAL).
FT DOMAIN 333 385 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 127 207 BY SIMILARITY.
FT LIPID 346 PALMITATE (POTENTIAL).
SQ SEQUENCE 385 AA; 5AD7E4C9B7077085 CRC64;

Query Match 19.0%; Score 390.5; DB 1; Length 385;
Best Local Similarity 26.9%; Pred. No. 8e-21;
Matches 104; Conservative 89; Mismatches 168; Indels 25; Gaps 9;

QY 1 METMGFMDDNATNTSTFSLVNLPHG-AHATSFPPNFSDYDMPLEDEDEDVNSRTFF 59
DB 1 MVLKMGVPGAEADENQTVEMKV-EPYGPHTT-----PRGELPPDPELIDSTKLV 51
QY 60 AAKIVGNALVGLMVGIGNFIIFIAALVRYKRLNLTLLIANLAISDFLVAIVCCPFE 119
DB 52 EVQVILILAYCSIIILGVGNSLVHVIKFSKRTVNFIFIANLAVADLLVNTLCPLFT 111
QY 120 MDYVYVRLQSWEGHGLVCTSYNLTSLVSVNALLAIAIDRYLAIVHPLRPMKQTA 179
DB 112 LTYTLNGE--WKMGVPLCHLVPAQGLAVQVSTLTITVIALDRHRCIVYHLESKISKIS 169
QY 180 TGLIALVMTYSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQOQLYKYS-YFLFI 238
DB 170 FLTIIGLAMGISALLASPLAIFREYSLIEIIPDFEIVACTEKWPGEEKSVGTYSLTL 229
QY 239 IEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRRTKTLVLMCILRAYVLCWA 298
DB 230 ILVYPLGIISFSTYRIMSKLNHVSFGAASDHYHQR---RHQMTKMLVCVVVFAVSWL 286
QY 299 PFYGTITVRDFFPTVFVKEKHYLTAFYIVCEIAMSNSMINTLCFTVVKNDTVKIF----- 353
DB 287 PLHAFQLAVDIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLLYGWNNSYKRAFLSAFR 345
QY 354 --KKIMLLHWKASYNGCKSSADLDLK 377
DB 346 CEORLDAIHSEVSMT-FRAKKNLEVK 370

RESULT 6
NY2R_HUMAN STANDARD; PRT; 381 AA.
AC Q49146; Q13281; Q13457; Q90E67;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).

```

GN NPY2R.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=96070760; PubMed=7592910;
RA Gerald C., Walker M.W., Vaysse P.J.-J., He C., Branchek T.A.,
RA Weinshank R.L.;
RT "Expression cloning and pharmacological characterization of a human
RT hippocampal neuropeptide Y/peptide YY Y2 receptor subtype.";
RL J. Biol. Chem. 270:26758-26761(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96226058; PubMed=8632753;
RA Gehlert D.R., Beavers L.S., Johnson D., Gackenhaimer S.L.,
RA Schober D.A., Gaski R.A.;
RT "Expression cloning of a human brain neuropeptide Y Y2 receptor.";
RL Mol. Pharmacol. 49:224-228(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96032678; PubMed=7559383;
RA Rose P.M., Fernandes P., Lynch J.S., Frazier S.T., Fisher S.M.,
RA Kodukula K., Kienzie B., Seethala R.;
RT "Cloning and functional expression of a cDNA encoding a human type 2
RT neuropeptide Y receptor.";
RL J. Biol. Chem. 270:22661-22664(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209788; PubMed=8643460;
RA Yan H., Yang J., Marasco J., Yamaguchi K., Brenner S., Collins F.,
RA Karbon W.;
RT "Cloning and functional expression of cDNAs encoding human and rat
RT pancreatic polypeptide receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4661-4665(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97131518; PubMed=8975716;
RA Ammar D.A., Eadie D.M., Wong D.J., Ma Y.-Y., Kolakowski L.F. Jr.,
RA Yang-Feng T.L., Thompson D.A.;
RT "Characterization of the human type 2 neuropeptide Y receptor gene
RT (NPY2R) and localization to the chromosome 4q region containing the
RT type 1 neuropeptide Y receptor gene.";
RL Genomics 38:392-398(1996).
RN [6]
RP SEQUENCE FROM N.A.
RA zastawny R.L.;
RL "Human neuropeptide Y Y2 receptor gene.";
CC Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE RANK
CC ORDER OF AFFINITY OF THIS RECEPTOR FOR PANCREATIC POLYPEPTIDES IS
CC PYY > NPY > PYY (3-36) > NPY (2-36) > [ILE-31, GLN-34] PP >
CC [LEU-31, PRO-34] NPY > PP, [PRO-34] PYY AND NPY FREE ACID.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS IN AMYGDALA, CORPUS CALLOSUM,
CC HIPPOCAMPUS AND SUBTHALAMIC NUCLEUS. ALSO DETECTABLE IN CAUDATE
CC NUCLEUS, HYPOTHALAMUS AND SUBSTANTIA NIGRA.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U36269; AAC50281.1; -;
DR EMBL; U42766; AAC04120.1; -;

DR EMBL; U32500; AAA93170.1; -;
DR EMBL; U42389; AAB07760.1; -;
DR EMBL; U50146; AAC51115.1; -;
DR EMBL; U76254; AAD00248.1; -;
DR PIR; I39187; I39187.
DR Gene; HGNC:7957; NPY2R.
DR MIM; 162642; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005246; F:calcium channel regulator activity; TAS.
DR GO; GO:0004983; F:neuropeptide Y receptor activity; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007193; P:G-protein signaling, adenylate cyclase inh.; TAS.
DR GO; GO:0007626; P:locomotory behavior; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 50 72 1 (POTENTIAL).
FT DOMAIN 73 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 104 2 (POTENTIAL).
FT DOMAIN 105 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 146 3 (POTENTIAL).
FT DOMAIN 147 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 187 4 (POTENTIAL).
FT DOMAIN 188 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 240 5 (POTENTIAL).
FT DOMAIN 241 268 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 269 291 6 (POTENTIAL).
FT DOMAIN 292 304 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 305 328 7 (POTENTIAL).
FT DOMAIN 329 381 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 123 203 BY SIMILARITY.
FT LIPID 342 342 PALMITATE (POTENTIAL).
FT CONFLICT 134 134 V -> A (IN REF. 3).
FT CONFLICT 172 172 A -> G (IN REF. 4).
FT CONFLICT 174 174 G -> R (IN REF. 4).
FT CONFLICT 202 202 A -> P (IN REF. 4).
FT CONFLICT 209 209 G -> A (IN REF. 4).
FT CONFLICT 248 248 N -> S (IN REF. 6).
FT CONFLICT 311 311 H -> Y (IN REF. 6).
SQ SEQUENCE 381 AA; 42731 MW; 7D018C0169597BC7 CRC64;
Query Match 18.9%; Score 387.5; DB 1; Length 381;
Best Local Similarity 29.5%; Pred. No. 1.3e-20;
Matches 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;
QY 47 DEDEDVTNRTFAAKIVIGMALVGMVCGIGNFIFIAALVRYKLRNLTLNLAIAI 106
DB 35 DPEPLDSTKLIEVQVLLIAYCSILLGVGNLSLVHVIVFKSMRTVNFNLAIV 94
QY 107 SDFLVAIVCCPFEMDYVYVQLSHEGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAI 166
DB 95 ADLLVNTLCPLFTLYTLGGE--WKMGVPLCHLVPAQAQGLAVQVSTITLVIALDRHRCI 152
QY 167 VHLPRPMKQOTAGLIAVWTVSILIAIPSAVFTTETVLVIVKSQKIFCGIWPVDQQ 226
DB 153 VYHLESIKRISPLIIGLAWISALLASPLAIFREYSLIEIIPDFEIVACTEKWPGEEK 212
QY 227 -LYKVSFLIFGIEFGVPTVMTLCYARISRELMFAVFGFQTEQIRKLRCKRTLV 285
DB 213 SIYGVTVLSLLLYLPLGIISFSYTSWKLKNHVSFGAANDHYHQ---RQKTRM 269
QY 286 LMCILTVLCWAPFYGTIVRDFPFTVYVFKHYLFAFYVECIAMNSKINTLCFTV 345
DB 270 LVCVVVFAVSWPLHAFQLAYDIDSOV-IDLKEYKLIFVFIHMCSTFANPLLYGWM 328
QY 346 KNDTVRYF 353
:: :: ::

```
Db 329 NSNYKAF 336
Best Local Similarity 27.28; Pred. No. 1.7e-20;
Matches 113; Conservative 82; Mismatches 148; Indels 73; Gaps 18;

RESULT 7
TLR2_DROME STANDARD; PRT; 519 AA.
AC P30975;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 01-JUL-1993 (Rel. 26, Last annotation update)
DE Tachykinin-like peptides receptor 99D (dtkr).
GN TAKR99D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RA MEDLINE=92007772; PubMed=1717263;
RA Li X.-J., Wolfgang W., Wu Y.-N., North R.A., Forte M.;
RT "Cloning, heterologous expression and developmental regulation of a
RT Drosophila receptor for tachykinin-like peptides.";
RL EMBO J. 10:3221-3229(1991).
CC -!- FUNCTION: PROBABLE RECEPTOR FOR TACHYKININ-LIKE PEPTIDES.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
CC -----
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CC -----
DR EMBL; X62711; CAA44595.1; -
DR FJIR; S17783; S17783.
DR FlyBase; FBgn0004622; Takr99D.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
DR Palmitate.
KW
FT DOMAIN 1 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 123 1 (POTENTIAL).
FT DOMAIN 124 134 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 135 155 2 (POTENTIAL).
FT DOMAIN 156 175 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 176 197 3 (POTENTIAL).
FT DOMAIN 198 217 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 218 238 4 (POTENTIAL).
FT DOMAIN 239 270 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 271 292 5 (POTENTIAL).
FT DOMAIN 293 324 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 325 346 6 (POTENTIAL).
FT DOMAIN 347 361 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 362 384 7 (POTENTIAL).
FT DOMAIN 385 519 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 471 481 GLY/SER-RICH.
FT CARBOHYD 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 174 254 BY SIMILARITY.
FT LIPID 399 PALMITATE (POTENTIAL).
SQ SEQUENCE 519 AA; 58480 MW; CACC51F50BE476B CRC64;
Query Match 18.9%; Score 387.5; DB 1; Length 519;

Best Local Similarity 27.28; Pred. No. 1.7e-20;
Matches 113; Conservative 82; Mismatches 148; Indels 73; Gaps 18;

OY 1 METTMGFMD-----NATNTST-----SFLSYLN--PHGATSPFP---NF 37
DB 1 MENRSDFEADDYGD1SWSNNNSWSTPAGVLFSAMSSVLSASNETPCRTLARSPYPPVSF 60
OY 38 SYS---DYDMPL-----DEDEDV-----TNSRFEA---AKIVIGHALVGLVCGIGNF 81
DB 61 NHSOTLSTQDPANGVEDAAEDAAASNETSGFAPVPMNQVLWSILFGGMVIVATGGNL 120
OY 82 IFTAALYRYKRLNLTLLIANLAISDFLVAIVCCPEMDYVYVYVQLSWEHGHVLCSTVN 141
DB 121 IVMIVMTTKRMRTVTNYFVNLISIADAVYSSLVNF--NYVYLDSDMPFGEFYCKLSQ 178
OY 142 YLRVSLYVSTNALLAIDRYLAIVHPLPRMKCQTATGLIALVWTVSVILIAIPSYFT 201
DB 179 FIAMLSICASVFTLMAISIDRYVAIRPLQPRSKRCNTAIAAVIWLASTLISCP----- 233
OY 202 TETVLVIVKSOE-----KIFCGQIW---PVDQQLYKRSYFLFIFGIEFGVPPVVTML 250
DB 234 ---NMIIYRTEVPYRGLSNRTVCYPMPOGPNHSTMESLYNLIILITFYFLPVSMTV 290
OY 251 CYARISRELWFKAVPGQTEOIRKRLCRKRTVLMCLITAYVLCWAPPYFTIIVRDEF 310
DB 291 TYSRVGIELWGSKTIGECTPRQVENRSRRVVMIVVYVLIIFAICWLPFHSFYIITSY 350
OY 311 PTV---FVKEKHVLTAFYIVCEIAMSNSMINTLCFTVVKNDTVKY-FKKIMLLHW 361
DB 351 PAITEAPFIQEL-YLAIYW-----LANSNSMINPIIYCYM-NSRFYGRF--MYFRW 398

RESULT 8
NY2R_MACMU STANDARD; PRT; 381 AA.
AC O9K74;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).
GN NPY2R.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184974; PubMed=11287088;
RA Gehlert D.R., Yang P., George C., Wang Y., Schober D.,
RA Gactenheimer S., Johnson D., Beavers L.S., Gadsdill R.A., Baez M.;
RT "Cloning and characterization of Rhesus monkey neuropeptide Y receptor
RT subtypes.";
RL Peptides 22:343-350(2001).
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC -----
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CC -----
DR EMBL; AF303090; AAG40772.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
```


DT 01-FEB-1996 (Rel. 33, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Proactin-releasing peptide receptor (PrRP receptor) (PrRP) (G protein-coupled receptor GPR10) (hGR3).

GN GPR10 OR GR3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=96115583; PubMed=8666380;

RA Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R., Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R., O'Dowd B.F., Docherty J.M.;

RA "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10, and GPR14, encoding receptors related to interleukin 8, neurotrophin Y, and somatostatin receptors.";

RT Genomics 29:335-344(1995).

RL [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=98268781; PubMed=9607765;

RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;

RA "A prolactin-releasing peptide in the brain.";

RT Nature 393:272-276(1998).

RN [3]

RN SEQUENCE FROM N.A.

RP Ozawa A., Yamada M., Sato T., Monden T., Hashimoto K., Sasaki T., Mori M.;

RA "Transcriptional regulation of the human prolactin-releasing peptide (PrRP) receptor gene by a dopamine agonist.";

RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

RN TISSUE SPECIFICITY

RP MEDLINE=99426652; PubMed=10498338;

RA Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Fujino M.;

RA "Tissue distribution of prolactin-releasing peptide (PrRP) and its receptor.";

RT Regul. Pept. 83:1-10(1999).

RL CC -1- FUNCTION: Receptor for prolactin-releasing peptide (PrRP).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Only detected in the pituitary gland.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: U32672; AAC50504.1; ..

DR EMBL: AB015745; BAA31159.1; ..

DR EMBL: AB048946; BAB83030.1; ..

DR Genew: HGNC:4464; GPR10.

DR MIW: 60895; ..

DR GO: GO:0005887; C: integral to plasma membrane; TAS.

DR GO: GO:0008198; F: neuropeptide receptor activity; TAS.

DR GO: GO:0007186; F: G-protein coupled receptor protein signalin. . .; TAS.

DR GO: GO:0007565; P: pregnancy; TAS.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSIN

DR PROSITE: PS00237; G-PROTEIN_RECEP_FL1; 1.

DR PROSITE: PS00262; G-PROTEIN_RECEP_FL2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 63 83 1 (POTENTIAL).

FT DOMAIN 84 101 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 102 122 2 (POTENTIAL).

FT DOMAIN 123 126 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 127 147 3 (POTENTIAL).

FT DOMAIN 148 175 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 176 196 4 (POTENTIAL).

FT DOMAIN 197 225 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 226 246 5 (POTENTIAL).

FT DOMAIN 247 276 6 (POTENTIAL).

FT TRANSMEM 277 297 7 (POTENTIAL).

FT DOMAIN 298 317 7 (POTENTIAL).

FT TRANSMEM 318 338 7 (POTENTIAL).

FT DOMAIN 339 369 BY SIMILARITY.

FT DISULFID 370 370 N-LINKED (GLNAC. . .) (POTENTIAL).

FT CARBOHYD 36 36 N-LINKED (GLNAC. . .) (POTENTIAL).

FT CARBOHYD 89 89 R -> P (IN REF. 1).

FT CONFLICT 170 175 RISLR -> ASRCA (IN REF. 1).

FT CONFLICT 194 194 A -> P (IN REF. 1).

SQ SEQUENCE 370 AA; 41106 MW; 08E9E57EBE6FC809 CRC64;

Query Match 18.08; Score 370; DB 1; Length 370;

Best Local Similarity 28.5%; Pred. No. 2.2e-19;

Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;

QY 21 SVLNPHGABATSPFNFSYSDYMDPLDEDEDVTNSRTFFAAKIVIGM--ALVIGIMLVCG- 77

DB 21 AVTTPANQSAEASAGSGSVAGADAPA-----VTFQSLQLVHQLKGLIVLLYSVVVGL 75

QY 78 IGNTFIFTAALVRYKKLNLTNLIANLAISDFLVAIVCCPFEMDYVVVROLSEHGHVLC 137

DB 76 VGNCLLVLTARVRLHNTVFNLIAGLSDVLMCTACVPLTL-AYAFEPGVVGGGLC 134

QY 138 TSVNKLRTSVLSYVSTNALLAIAIDRYLAIVHPLPRMKCOTATGLIALVTVSILIAIPS 197

DB 135 HCVFELQPVTVVSVFTLTITANDRVTVVHPLRRISLSLSAYAVLAIALSVALPALA 194

QY 198 AYTFTTVLVIVKQKIFCGQIMPVDQ---QLYKSYFLFIFGIEFVGVPVVTMTLCYAR 254

DB 195 A---VHTYHVELKPHDVRCLKEEFMGSGORQLYAWGILL---VTYLLPLLVLLSYVR 247

QY 255 ISRELKFAVPGFQTEQIRKELRC-REKTVLVMCLITAVVLCWAPYGTIVRDFPTV 313

DB 248 VSVKLRNVPGCVTQSQADWDARRRTFCLLVVVVVVAVCVMLPHVFNLLRLDLP-- 305

QY 314 FVREKHYLT--AFYIVE--C--IAMSMSMINTLCFTVTKNDTVYFKKIMLLHW 361

DB 306 -----HAIDPVAFGLVQLLCHLWLAASACYNPFYIAML-HDSFRELKLLVAW 353

RESULT 11

GP10_RAT

ID GP10_RAT STANDARD; PRT; 370 AA.

AC Q64121;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Proactin-releasing peptide receptor (PrRP receptor) (PrRP) (G protein-coupled receptor GPR10) (UHR-1).

GN GPR10.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Hypothalamus;

RX MEDLINE=95251659; PubMed=7733930;

RA Welch S.K., O'Hara B.F., Kilduff T.S., Heller H.C.;

RT "Sequence and tissue distribution of a candidate G-coupled receptor cloned from rat hypothalamus.";

RL Biochem. Biophys. Res. Commun. 209:606-613(1995).

```

RN  [2]
RP  TISSUE SPECIFICITY.
RX  MEDLINE=99426652; PubMed=10498338;
RA  Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
RA  Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
RA  Sumino Y., Fujino M.;
RT  "Tissue distribution of prolactin-releasing peptide (PrRP) and its
RL  receptor.";
RL  Regul. Pept. 83:1-10(1999).
CC  -1- FUNCTION: Receptor for prolactin-releasing peptide (PrRP).
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in
CC  pituitary, cerebellum, and hypothalamus.
CC  -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; S77867; AB34129.1; -.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODOPSN.
DR  PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR  PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein.
FT  DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 63 83 1 (POTENTIAL).
FT  DOMAIN 84 101 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 102 121 2 (POTENTIAL).
FT  DOMAIN 123 126 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 127 147 3 (POTENTIAL).
FT  DOMAIN 148 175 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 176 196 4 (POTENTIAL).
FT  DOMAIN 197 223 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 224 244 5 (POTENTIAL).
FT  DOMAIN 245 276 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 277 297 6 (POTENTIAL).
FT  DOMAIN 298 317 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 318 338 7 (POTENTIAL).
FT  DISULFD 134 211 CYTOPLASMIC (POTENTIAL).
FT  CARBOHYD 27 27 BY SIMILARITY.
FT  SEQUENCE 370 AA; 41160 MW; 8E5E689D127CB2C CRC64;
SQ  -----
Query Match 17.9%; Score 367.5; DB 1; Length 370;
Best Local Similarity 30.1%; Pred. No. 3.3e-19;
Matches 91; Conservative 67; Mismatches 121; Indels 23; Gaps 10;
QY 69 LVGIMLVCG-IGNFIFIAALVYKRLNLTNLIANTLAISDFLVAIVCCPFEMDYVVYRQ 127
DB 66 LYSIVVYVGLVGNCLLVLIARVRLHNTNFIIGNLALSVDVLMCAACVPLT-AYAFEP 124
QY 128 LSWEHGHVLCRSVNYLRTVSVLYSVNALLAIDRYLAIVHPRLMKCQATGLIALVW 187
DB 125 RCWVFGGGLCHLVFPLOPVTVVSVFTLTITANDRYVVLVPLRRISLKLAYAVLGIV 184
QY 188 TVSILIAIPSYFTTETVLVIVKSEKIFCGQINPVDQOLYKSYFLFIFGI---EFVGP 244
DB 185 ALSAVLALPAA---VHTYHVELKHPDVRCEEFNGSQE---RROIIYAWGLLLGTLLP 237
QY 245 VVTWTLCTVARSRELWFAVFGFQTEQTKRLRC-RRRTVLVLMCLTAYVLCWAPFVGF 303
DB 238 LLAILLSTVRSVSKLRNRPVGSVTSQADWDRAARRRTFCLLVVVVVVFCALCWLPLHIF 297
QY 304 TIVRDFEFTVFVKRHYLTAFFIVE--C--TAMSNMINTLCFVTVKNDTVKYEKKIMLL 359
DB 298 NLIRDLDPRAIDP-----YAFGLVQLLCHWLAMSSACTNPFIIAWL-HDSPREELRKMILL 351

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QY 360 HW 361
DB 352 SW 353
RESULT 12
NK2R_MOUSE STANDARD; PRT; 384 AA.
ID NK2R_MOUSE
AC P30549; 1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Substance-K receptor (SKR) (Neurokinin A receptor) (NK-2 receptor)
DE (NK-2R).
GN TACR2 OR TAC2R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Intestine;
RX MEDLINE=92137253; PubMed=1370937;
RA Sundelin J.B., Provvedini D.M., Wahlestedt C.R., Laurell H.,
RA Pohl J.S., Peterson P.A.;
RT "Molecular cloning of the murine substance K and substance P receptor
RT genes.";
RL Eur. J. Biochem. 203:625-631(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE
CC SUBSTANCE K (NEUROKININ A). IT IS ASSOCIATED WITH G PROTEINS THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO
CC TACHYKININS IS: SUBSTANCE K > NEUROKININ K > SUBSTANCE P.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X62933; CAA44706.1; -.
DR  PIR; S20303; S20303.
DR  HSP; P02699; IF88.
DR  MGD; MGI:98477; Tacr2.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODOPSN.
DR  PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR  PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein;
KW  phosphorylation; Lipoprotein; Palmitate.
FT  DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 33 56 1 (POTENTIAL).
FT  DOMAIN 57 69 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 70 90 2 (POTENTIAL).
FT  DOMAIN 91 107 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 108 129 3 (POTENTIAL).
FT  DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 150 170 4 (POTENTIAL).
FT  DOMAIN 171 196 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 197 218 5 (POTENTIAL).
FT  DOMAIN 219 251 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 252 272 6 (POTENTIAL).
FT  DOMAIN 273 290 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 291 310 7 (POTENTIAL).
FT  DOMAIN 311 384 CYTOPLASMIC (POTENTIAL).
FT  CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).

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Db 175 -PSRVCMIEPHEPNRTYKAYHICVTLVLYFLPLVIGYAVTWGTLWASIPGDS 233
Qy 270 EQIKRLRCRKRLVLMCLTAVVLCWAPPYGFIVRDFPFTVVK---EKHYLTAFYI 326
Db 234 DRYHEQYSAKRYKVMVIVVCTFAICWLPFHVFFLLPYNPDLKFKFQQVYLASMW- 292
Qy 327 VECIAMSNTLCFVTVKND 348
Db 293 ---LAMSTWYNIYCCCL-ND 310

RESULT 14
ID NK1R_MOUSE STANDARD; PRT; 407 AA.
AC P30548;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Substance-P receptor (SPR) (NK-1 receptor) (NK-1R).
OS TACR1 OR TAC1R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=92137253; PubMed=1370937;
RA Sundelin J.B., Provvedini D.M., Wahlestedt C.R., Laurell H.,
RA Pohl J.S., Peterson P.A.;
RT "Molecular cloning of the murine substance K and substance P receptor
RT genes.";
RL Eur. J. Biochem. 203:625-631(1992).
RN [2]
RP SEQUENCE OF 53-290 FROM N.A.
RC STRAIN=CBA; TISSUE=Brain, and T-cell;
RX MEDLINE=94165478; PubMed=8120392;
RA Cook G.A., Elliott D., Metwalli A., Blum A.M., Sandor M., Lynch R.,
RA Weinstein J.V.;
RT "Molecular evidence that granuloma T lymphocytes in murine
RT schistosomiasis mansoni express an authentic substance P (NK-1)
RT receptor.";
RL J. Immunol. 152:1830-1835(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE
CC SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO
CC TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X62934; CAA44707.1; -
CC DR EMBL; L27828; AAA17892.1; -
CC DR EMBL; L27826; AAA17891.1; -
CC DR PIR; S20304; S20304.
CC DR MGD; MGI:98475; Tacrl.
CC DR InterPro; IPR000276; GPCR_Rhodopsn.
CC DR Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR00237; GPCRHHODOPSN.
CC DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
CC DR PROSITE; PS00237; G_PROTEIN_RECP_FL_2; 1.
CC DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
CC DR G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Lipoprotein; Palmitate.

```

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FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 32 54 1 (POTENTIAL).
FT DOMAIN 55 64 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 106 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 107 128 3 (POTENTIAL).
FT DOMAIN 129 148 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 149 169 4 (POTENTIAL).
FT DOMAIN 170 194 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 195 219 5 (POTENTIAL).
FT DOMAIN 220 248 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 283 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 284 308 7 (POTENTIAL).
FT DOMAIN 309 407 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 105 180 BY SIMILARITY.
FT LIPID 322 322 PALMITATE (POTENTIAL).
SQ SEQUENCE 407 AA; 45186D475A6659A0 CRC64;

Query Match 17.5%; Score 360.5; DB 1; Length 407;
Best Local Similarity 25.5%; Pred. No. 1.1e-18;
Matches 82; Conservative 84; Mismatches 129; Indels 27; Gaps 10;

Qy 41 DYDMLDIED-----EDVTSNRTFFAA--KIVIGMALVIGIMLVCG-IGNFIFTAALVRK 91
Db 2 DNVLPVDSLDLPNTSTNTSESNQFQVQWQIVLWAAAYVIVTVSVGVNVMVWIIAHLK 61
Qy 92 KLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVRLSMEHGHVLTCTSVNLTSLTVS 151
Db 62 RMRVTNIVFLVNLAFACACMAFNTVVFYAV--HNVVYGLFYCKFHFNFPIAALFAS 119
Qy 152 TNALLAIDRYLAIVHPLRPMKQCTATGLIALVWTVSILIALPSAYF-TTETVLVYVK 210
Db 120 IYSMTAVAFQRYMAIHPLQPLRSATATKVIVFWLALLAFPGGYSTTETM----- 174
Qy 211 SOKIFGQGIWPV-DQOLYKSYFLFIEFGIEFVGVVMTFLCYARISRELWKAIVPGQT 269
Db 175 -PSRVCMIEPHEPNRTYKAYHICVTLVLYFLPLVIGYAVTWGTLWASEIPGDS 233
Qy 270 EQIKRLRCRKRLVLMCLTAVVLCWAPPYGFIVRDFPFTVVK---EKHYLTAFYI 326
Db 234 DRYHEQYSAKRYKVMVIVVCTFAICWLPFHVFFLLPYNPDLKFKFQQVYLASMW- 292
Qy 327 VECIAMSNTLCFVTVKND 348
Db 293 ---LAMSTWYNIYCCCL-ND 310

RESULT 15
ID NK2R_RABIT STANDARD; PRT; 384 AA.
AC P79218;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Substance-K receptor (SKR) (Neurokinin A receptor) (NK-2 receptor)
DE (NK-2R).
DE TACR2 OR TAC2R.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pulmonary artery;
RX MEDLINE=95182423; PubMed=7877137;
RA Aharony D., Little J., Thomas C., Powell S., Downey-Jones M.,
RA Graham A.;
RT "Isolation and characterization of neurokinin A receptor cDNAs from
RT guinea-pig lung and rabbit pulmonary artery.";
RL J. Recept. Res. 14:399-421(1994).

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:50:42 ; Search time 20 Seconds
(without alignments)
831.408 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTMGPMDDNATNTSTFL.....LDLKTICMPATEVDCIRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1766 | 85.9 | 384 | 2 | US-08-833-226-2 |
| 2 | 401.5 | 19.5 | 381 | 2 | US-08-687-355A-4 |
| 3 | 401.5 | 19.5 | 381 | 4 | US-09-407-367-4 |
| 4 | 395.5 | 19.2 | 381 | 2 | US-08-687-355A-6 |
| 5 | 395.5 | 19.2 | 381 | 4 | US-09-407-367-6 |
| 6 | 387.5 | 18.9 | 381 | 1 | US-08-192-288-2 |
| 7 | 387.5 | 18.9 | 381 | 2 | US-08-687-355A-2 |
| 8 | 387.5 | 18.9 | 381 | 4 | US-09-200-673-16 |
| 9 | 387.5 | 18.9 | 381 | 4 | US-09-407-367-2 |
| 10 | 384.5 | 18.7 | 381 | 4 | US-08-876-708A-2 |
| 11 | 370 | 18.0 | 370 | 3 | US-08-513-974B-26 |
| 12 | 370 | 18.0 | 370 | 3 | US-08-513-974B-323 |
| 13 | 370 | 18.0 | 370 | 3 | US-09-172-353-5 |
| 14 | 370 | 18.0 | 370 | 3 | US-08-776-971-21 |
| 15 | 370 | 18.0 | 370 | 3 | US-08-776-971-104 |
| 16 | 370 | 18.0 | 370 | 4 | US-09-799-955-5 |
| 17 | 370 | 18.0 | 370 | 4 | US-09-461-436B-26 |
| 18 | 369.5 | 18.0 | 369 | 3 | US-09-172-353-6 |
| 19 | 369.5 | 18.0 | 369 | 4 | US-09-799-955-6 |
| 20 | 368.5 | 18.0 | 369 | 4 | US-09-170-496D-26 |
| 21 | 368.5 | 17.9 | 369 | 4 | US-09-170-496D-178 |
| 22 | 368.5 | 17.9 | 370 | 3 | US-08-776-971-140 |
| 23 | 367.5 | 17.9 | 370 | 3 | US-09-172-353-7 |
| 24 | 367.5 | 17.9 | 370 | 4 | US-09-799-955-7 |
| 25 | 363.5 | 17.7 | 370 | 3 | US-09-172-353-2 |
| 26 | 363.5 | 17.7 | 370 | 3 | US-09-172-353-3 |
| 27 | 363.5 | 17.7 | 370 | 4 | US-09-799-955-2 |

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| 28 | 363.5 | 17.7 | 370 | 4 | US-09-799-955-3 | Sequence 3, Appli |
| 29 | 362.5 | 17.6 | 372 | 1 | US-07-937-609-20 | Sequence 20, Appl |
| 30 | 362.5 | 17.6 | 372 | 3 | US-08-029-170-20 | Sequence 20, Appl |
| 31 | 362.5 | 17.6 | 407 | 5 | PCT-US92-06532-7 | Sequence 7, Appli |
| 32 | 357.5 | 17.4 | 407 | 2 | US-08-390-000A-6 | Sequence 6, Appli |
| 33 | 356.5 | 17.3 | 311 | 1 | US-07-701-935-26 | Sequence 26, Appl |
| 34 | 356.5 | 17.3 | 407 | 1 | US-08-117-965-26 | Sequence 26, Appl |
| 35 | 356.5 | 17.3 | 407 | 5 | PCT-US92-06532-3 | Sequence 3, Appli |
| 36 | 351 | 17.1 | 402 | 3 | US-08-846-704-4 | Sequence 3, Appli |
| 37 | 351 | 17.1 | 402 | 4 | US-08-462-509B-2 | Sequence 2, Appli |
| 38 | 351 | 17.1 | 402 | 5 | PCT-US95-05616-2 | Sequence 2, Appli |
| 39 | 351 | 17.1 | 425 | 3 | US-08-846-704-2 | Sequence 2, Appli |
| 40 | 351 | 17.1 | 425 | 4 | US-09-479-128-2 | Sequence 2, Appli |
| 41 | 350 | 17.0 | 369 | 4 | US-08-462-509B-4 | Sequence 4, Appli |
| 42 | 350 | 17.0 | 369 | 5 | PCT-US95-05616-4 | Sequence 4, Appli |
| 43 | 350 | 17.0 | 372 | 4 | US-08-462-509B-6 | Sequence 6, Appli |
| 44 | 350 | 17.0 | 377 | 5 | PCT-US95-05616-6 | Sequence 6, Appli |
| 45 | 350 | 17.0 | 389 | 2 | US-08-846-705-2 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-08-833-226-2
; Sequence 2, Application US/08833226
; Patent No. 5891720
; GENERAL INFORMATION:
; APPLICANT: Moore, Karen
; APPLICANT: Nagle, Deborah
; APPLICANT: Woolf, Elizabeth
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,226
; FILING DATE: 17-APR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-833-226-2

Query Match 85.9%; Score 1766; DB 2; Length 384;
Best Local Similarity 87.4%; Pred. No. 1.5e-168;
Matches 334; Conservative 20; Mismatches 28; Indels 0; Gaps 0;
QY 12 ATNTSTSELSNPEGAHATSPFNFSYSDYDMPLEDEDTNSRTFFAAKIVIGALVG 71
DB 3 AQNGNTSFPTNPNPODHASSLSFNFSYDGYDLPDEDEDTMTKTRTFFAAKIVIGIALAG 62

QY 72 IMLVCGIGNFIFAALRYKKLRNLTNLLIANLAISDFLVAIVCCPFEMDYVVRQLSWE 131
 DB 63 IMLVCGIGNFIFAALRYKKLRNLTNLLIANLAISDFLVAIVCCPFEMDYVVRQLSWE 122
 QY 132 HGVVLCTSVNLTSLVYSTNALLAIAIDRYLAIVHPLRPMKOTATGLIALVTVTSI 191
 DB 123 HGVLCASVNLRTVSLVYSTNALLAIAIDRYLAIVHPLRPMKOTATGLIALVTVTSI 182
 QY 192 LIAIPSAVFTTETVLVIVKQEKIFCGQIWPVDQQLYKSYFLFIFGIEFVGPVVTMLC 251
 DB 183 LIAIPSAVFTTETVLVIVKQEKIFCGQIWPVDQQLYKSYFLFIFGIEFVGPVVTMLC 242
 QY 252 YARISRELWFKAVPGFQEQIRKRLCRKTVLVMCILTAIVLCWAPFYGFTIVRDEFF 311
 DB 243 YARISRELWFKAVPGFQEQIRKRLCRKTVLVMCILTAIVLCWAPFYGFTIVRDEFF 302
 QY 312 TVFVKEKHYLTAFYIVECIAMSNTLCFVTVKNDTVKYFKKIMLHWKASNGGKSS 371
 DB 303 TVFVKEKHYLTAFYIVECIAMSNTLCFVTVKNDTVKYFKKIMLHWKASNGGKSS 362
 QY 372 ADLDTKICMPATEEVDICIRLK 393
 DB 363 ADLDTKICMPATEEVDICIRLK 384

RESULT 2

US-08-687-355A-4
 ; Sequence 4, Application US/08687355A
 ; Patent No. 5989834
 ; GENERAL INFORMATION:
 ; APPLICANT: Synaptic Pharmaceutical Corporation
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
 ; TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/687,355A
 ; FILING DATE: No. 5989834ember 26, 1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPW/MAT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 381 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-687-355A-4

Query Match 19.5%; Score 401.5; DB 2; Length 381;
 Best Local Similarity 28.6%; Pred. No. 4.4e-32;
 Matches 98; Conservative 83; Mismatches 147; Indels 15; Gaps 6;
 QY 43 DMPLEDEDVTSRTEFAAKIVIGMALVGMVLCGIGNFIFAALRYKKLRNLTNLLIA 102
 DB 31 ELPDPPELIDSKLVEVQVLLAYCSILLGVGNSLIVHVKFKSKRVTNFFFA 90

QY 103 NLAISDFLVAIVCCPFEMDYVVRQLSWEHGVVLCTSVNLTSLVYSTNALLAIAIDR 162
 DB 91 NLAIVADLVNTLCLPFTLTTLTNGE--WKMGVPVLCVHVPYAOGLAVQVSTITLTVALDR 148
 QY 163 YLAIVHPLRPMKOTATGLIALVTVTSIILIAIPSAVFTTETVLVIVKQEKIFCGQIWP 222
 DB 149 HRCIVTHLESKISKQISFLIIGLAWGSALLASPLAIFREYSLSLIEIIPDFEIVACTEKP 208
 QY 223 VDQQLYKSYFLFIFGIEFVGPVVTMLCYARISRELWFKAVPGFQEQIRKRLCRK 281
 DB 209 GEKSVTVGTVSLTLLILLYPLGIISFSYTRIMSKLXNHVSPGAASDRYHOR---RHK 265
 QY 282 TVLVLMCILTAIVLCWAPFYGFTIVRDEFFTVFVKEKHYLTAFYIVECIAMSNTMLC 341
 DB 266 TTKMLCVVVFVAVSWLPLHAFQVLAVIDISHV-LDLKEYKLIFTVPHILAMGSTFANPLL 324
 QY 342 FTVTKNDTVKYF-----KKIMLHWKASNGGKSSADLKL 377
 DB 325 YGMNSNYRKAFLSAERCEORLDAIHSEVSMT-FKAKKNLEVK 366

RESULT 3

US-09-407-367-4
 ; Sequence 4, Application US/09407367
 ; Patent No. 6420532
 ; GENERAL INFORMATION:
 ; APPLICANT: Christophe P.G. Gerald, et al.
 ; TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COI
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/407,367
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 381 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-407-367-4

Query Match 19.5%; Score 401.5; DB 4; Length 381;
 Best Local Similarity 28.6%; Pred. No. 4.4e-32;
 Matches 98; Conservative 83; Mismatches 147; Indels 15; Gaps 6;

QY 43 DMPLEDEDVTSRTEFAAKIVIGMALVGMVLCGIGNFIFAALRYKKLRNLTNLLIA 102
 DB 31 ELPDPPELIDSKLVEVQVLLAYCSILLGVGNSLIVHVKFKSKRVTNFFFA 90
 QY 103 NLAISDFLVAIVCCPFEMDYVVRQLSWEHGVVLCTSVNLTSLVYSTNALLAIAIDR 162
 DB 91 NLAIVADLVNTLCLPFTLTTLTNGE--WKMGVPVLCVHVPYAOGLAVQVSTITLTVALDR 148

[illegible]

RESULT 4
 US-08-687-355A-6
 : Sequence 6, Application US/08687355A
 : Patent No. 5989834
 : GENERAL INFORMATION:
 : APPLICANT: Synaptic Pharmaceutical Corporation
 : TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
 : TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
 : NUMBER OF SEQUENCES: 27
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Cooper & Dunham LLP
 : STREET: 1185 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10036
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/687,355A
 : FILING DATE: No. 5989834ember 26, 1996
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: White, John P.
 : REGISTRATION NUMBER: 28,678
 : REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPH/MAT
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 212-278-0400
 : TELEFAX: 212-391-0525
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 381 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-687-355A-6

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223 VDOOLYKYS-YFLIFGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKLRCRRK 281
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
209 GEKSVYGVYISLTLILVPLGLIISFSYTRISWKLKNHVSFGAASDHYHQ- --RHK 265
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
282 TVLVMCILTAAYVLWCAPFYGFIVRDFPTVFVKEKHYLTAFYIVECIAMNSMINTLC 341
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
266 MTKMLVCVVVFAVSNLPLHAFQLAVNDIDSHV-LDLKEYKLIFVFIHIAIAMSCTFANPLL 324
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
342 FVTXKNDTVKYF-----KKIMLLHWKASYNGKSSADLDLK 377
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
325 YGMWNSNYRKAFLSAFRCQRLDAIHSEVSMT-FKAKKNLEVK 366
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

RESULT 5
US-09-407-367-6
; Sequence 6, Application US/09407367
; Patent No. 6420532
; GENERAL INFORMATION:
; APPLICANT: Christophe P.G. Gerald, et al.
; TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC CO
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,367
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-407-367-6

Query Match 19.2%; Score 395.5; DB 4; Length 381;
Best Local Similarity 28.3%; Pred. No. 1.8e-31;
Matches 97; Conservative 83; Mismatches 148; Indels 15; Gaps 6;

QY 43 DMPLEDEDVYNSRTFFPAKTVIGNALVIGMLVCYCGINFIPTAALVRYKKLENLNLIA 102
DB 31 ELPPDPELIDSTKLVEVQVLLAYLACISILLGVGNSVLIVHVVKFSMTVTVNFIA 90
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 103 NLAISDFEIVAVCCPFEDMYVVRQLSHEGHVLCITSVNYLRTSVLSYTNALLAIAIDR 162
DB 91 NLAVDLLVNTLCLPFTLTLYLWGE--NKMGPVLCHLYPAQGLAVQVSTLTITVIALDR 148
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 163 YLAIVHLPRMKQOTATGLTALVWTVSILIAIPSAYTTEVTLVIVVKSQKIFCGQIWP 222
DB 149 HRCIVYHLESKIQISPLIIGLAWGVSAIIASPLAIFREYSLSIIRIPDFEIVACTEKP 208
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 223 VDOOLYKYS-YFLIFGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKLRCRRK 281
DB 209 GEKSVYGVYISLTLILVPLGLIISFSYTRISWKLKNHVSFGAASDHYHQ- --RHK 265
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
282 TVLVMCILTAAYVLWCAPFYGFIVRDFPTVFVKEKHYLTAFYIVECIAMNSMINTLC 341
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

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Db 266 MTKMLVCVVVFAVSWLPLHAFQALAVDIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLL 324
QY 342 FVTYKNDTVKYF-----KKMLLHWKASVNGKGSSADLDK 377
Db 325 YGWNNSYRKAFSLAFRCERQRLDAIHSEVSWT-FAKKNLEVK 366

RESULT 6

US-08-192-288-2
; Sequence 2, Application US/08192288
; Patent No. 5545549
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTOR AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,288
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44742/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-192-288-2

Query Match 18.9%; Score 387.5; DB 1; Length 381;
Best Local Similarity 29.5%; Pred. No. 1.1e-30;
Matches 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;
QY 47 DEDEDVTSRTEFAAKIVIGMALVGMVCGIGNFTIAALVRYKKRLNLTLLIANLAI 106
Db 35 DPEPLIDSTKLEVVQWLILAYCSIIILGVGNSLVHVIWIKFKSMRTVTNFFANLAV 94
QY 107 SDFLVAIVCCPFEMDYVVRQLSWEGHVLCTSVNTLRVSLVSTNALLAIDRYLAI 166
Db 35 DPEPLIDSTKLEVVQWLILAYCSIIILGVGNSLVHVIWIKFKSMRTVTNFFANLAV 94
QY 167 VHLPRMKQOTATGLIALVMTVSYLIIAIPSAVFTTETVLVIVKSOEIKFCQIWPVDOQ 226
Db 95 ADLLVNTLCPLFTLTLMGE--WKMGVPLCHLVPAQGLAVQVSTITLTVALDRHRCI 152
QY 167 VHLPRMKQOTATGLIALVMTVSYLIIAIPSAVFTTETVLVIVKSOEIKFCQIWPVDOQ 226
Db 153 VYHLESKISRISFLIIGLAWGISALLASPLAIFREYSLEIIPDFEIVACTEKWPGEK 212
QY 227 -LYKSYFLIFGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLV 285
Db 213 SIYGTVYSLSLILVPLPLGIISFSTYTRWSLKNHVSFGAANDRYHQR---RQKTTKM 269
QY 227 -LYKSYFLIFGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLV 285
Db 213 SIYGTVYSLSLILVPLPLGIISFSTYTRWSLKNHVSFGAANDRYHQR---RQKTTKM 269

QY 286 LMCILTAYVLCNAPYVGGTIVRDFFPTVVRKHKHLYTAFYIVECIAMNSMINTLCFTTV 345
Db 270 LVCVVVFAVSWLPLHAFQALAVDIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLL 328
QY 346 KNDTVKYF 353
Db 329 NSNYRKAF 336

RESULT 7

US-08-687-355A-2
; Sequence 2, Application US/08687355A
; Patent No. 5989834
; GENERAL INFORMATION:
; APPLICANT: Synaptic Pharmaceutical Corporation
; TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,355A
; FILING DATE: No. 5989834ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPW/MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-355A-2

Query Match 18.9%; Score 387.5; DB 2; Length 381;
Best Local Similarity 29.5%; Pred. No. 1.1e-30;
Matches 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;
QY 47 DEDEDVTSRTEFAAKIVIGMALVGMVCGIGNFTIAALVRYKKRLNLTLLIANLAI 106
Db 35 DPEPLIDSTKLEVVQWLILAYCSIIILGVGNSLVHVIWIKFKSMRTVTNFFANLAV 94
QY 107 SDFLVAIVCCPFEMDYVVRQLSWEGHVLCTSVNTLRVSLVSTNALLAIDRYLAI 166
Db 95 ADLLVNTLCPLFTLTLMGE--WKMGVPLCHLVPAQGLAVQVSTITLTVALDRHRCI 152
QY 167 VHLPRMKQOTATGLIALVMTVSYLIIAIPSAVFTTETVLVIVKSOEIKFCQIWPVDOQ 226
Db 153 VYHLESKISRISFLIIGLAWGISALLASPLAIFREYSLEIIPDFEIVACTEKWPGEK 212
QY 227 -LYKSYFLIFGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLV 285
Db 213 SIYGTVYSLSLILVPLPLGIISFSTYTRWSLKNHVSFGAANDRYHQR---RQKTTKM 269
QY 286 LMCILTAYVLCNAPYVGGTIVRDFFPTVVRKHKHLYTAFYIVECIAMNSMINTLCFTTV 345
Db 270 LVCVVVFAVSWLPLHAFQALAVDIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLL 328

QY 346 KNDTVKYF 353
Db 329 NSNYRKAF 336

RESULT 8

US-09-200-673-16

; Sequence 16, Application US/09200673A

; Patent No. 6316203

; GENERAL INFORMATION:

; APPLICANT: Gerald, Christophe P.G.

; APPLICANT: Weinschank, Richard L.

; APPLICANT: Walker, Mary W.

; APPLICANT: Branchek, Theresa

; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful

; TITLE OF INVENTION: In Such Methods, and DNA Encoding A Hypothalamic

; FILE REFERENCE: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)

; CURRENT FILING DATE: 1998-11-25

; CURRENT FILING DATE: 1998-11-25

; EARLIER APPLICATION NUMBER: 08/566,096

; EARLIER FILING DATE: 1995-12-01

; EARLIER APPLICATION NUMBER: 08/349,025

; EARLIER FILING DATE: 1994-12-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 381

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-200-673-16

Query Match

Best Local Similarity 18.9%; Score 387.5; DB 4; Length 381;

Matches: 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;

QY 47 DEDEDVNSRTFFAAKIVIGMALVGVGIMLVGIGNFIFIAALVRYKKRLNLTLLIANLAI 106

Db 35 DPEPELIDSTKLEIVQVVLILAYCSIIILGVIGNSLVHVIVKFSKMRVTNFFIANLAV 94

QY 107 SDFLVAIVCCPFENDYVYVROLSEHGHVLTCTSVNYLRTVSLVSTNALLAIDRYLAI 166

Db 95 ADLLVNTLCPLFTLTITLAGE--WKMGVPLCHLVPAQGLAVQVSTITLTVIALDRHRCI 152

QY 167 VHLPRMKCOTATGLIALVWTVSIIILAIIPSAFYFTTETVLVIVKSOEIKFCGOINPVDQO 226

Db 153 VYHLESKISKRIISFLIIGLAWGISALLASPLAIFREYSLIEIIPDFEIVACTEKWPGEK 212

QY 227 -LYKSYELFIFGIEFVGPVVTWTLCYARISRELWFKAVPGFQTEIRKRLCRKRTVLV 285

Db 213 SIYGTVYSLSLILYVPLGIISFYSTRIMSKLNHVSPGAANDHYHQR--RQKTTKM 269

QY 286 LMCILTAYVLCWAPFYGFTIVRDFPFTVYVYKHYLTAFYIVECIAMSNMINTLCFVTV 345

Db 270 LVCVVVFAVSWLPLHAFQLAVIDSQV-LDLKEYKLIFTVPHIIMCSTFANPLLYGWM 328

QY 346 KNDTVKYF 353

Db 329 NSNYRKAF 336

RESULT 9

US-09-407-367-2

; Sequence 2, Application US/09407367

; Patent No. 6420532

; GENERAL INFORMATION:

; APPLICANT: Christophe P.G. Gerald, et al.

; TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COMPO

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,367
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-407-367-2

Query Match

Best Local Similarity 18.9%; Score 387.5; DB 4; Length 381;

Matches: 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;

QY 47 DEDEDVNSRTFFAAKIVIGMALVGVGIMLVGIGNFIFIAALVRYKKRLNLTLLIANLAI 106

Db 35 DPEPELIDSTKLEIVQVVLILAYCSIIILGVIGNSLVHVIVKFSKMRVTNFFIANLAV 94

QY 107 SDFLVAIVCCPFENDYVYVROLSEHGHVLTCTSVNYLRTVSLVSTNALLAIDRYLAI 166

Db 95 ADLLVNTLCPLFTLTITLAGE--WKMGVPLCHLVPAQGLAVQVSTITLTVIALDRHRCI 152

QY 167 VHLPRMKCOTATGLIALVWTVSIIILAIIPSAFYFTTETVLVIVKSOEIKFCGOINPVDQO 226

Db 153 VYHLESKISKRIISFLIIGLAWGISALLASPLAIFREYSLIEIIPDFEIVACTEKWPGEK 212

QY 227 -LYKSYELFIFGIEFVGPVVTWTLCYARISRELWFKAVPGFQTEIRKRLCRKRTVLV 285

Db 213 SIYGTVYSLSLILYVPLGIISFYSTRIMSKLNHVSPGAANDHYHQR--RQKTTKM 269

QY 286 LMCILTAYVLCWAPFYGFTIVRDFPFTVYVYKHYLTAFYIVECIAMSNMINTLCFVTV 345

Db 270 LVCVVVFAVSWLPLHAFQLAVIDSQV-LDLKEYKLIFTVPHIIMCSTFANPLLYGWM 328

QY 346 KNDTVKYF 353

Db 329 NSNYRKAF 336

RESULT 10

US-08-876-798A-2

; Sequence 2, Application US/08876798A

; Patent No. 6355478

; GENERAL INFORMATION:

; APPLICANT: Baez, Melvyn

; APPLICANT: Yang, Peiyi

; TITLE OF INVENTION: RHESUS MONKEY NEUROPEPTIDE Y RECEPTOR

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eli Lilly and Company

; STREET: Lilly Corporate Center

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: U.S.A.

; ZIP: 46285

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876,798A
; FILING DATE: 16-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)276-0756
; TELEFAX: (317)276-2763
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-876-798A-2

Query Match 18.7%; Score 384.5; DB 4; Length 381;
Best Local Similarity 29.2%; Pred. No. 2.2e-30;
Matches 90; Conservative 74; Mismatches 137; Indels 7; Gaps 4;

QY 47 DEDEDVNSRTFFAAKIVGMLVCGIGNFIFIAALVRYKKLNLIANLAI 106
Db 35 DPPELIDSTKLEQVGVILAYCSITLLGVNSLVHVIKFKSMRTVNFNLANLV 94
QY 107 SDFNAIVCCPFEMDYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 166
Db 95 ADLVVNTLCPLFTLYTLAGE--WKMGPVLCVLAQGLAVQVSTITLTALDRHRCI 152
QY 167 VHPRLPRMCKOTATGIALVWTVSILAIPTSAFTTEVTVLVKSOEIFCGQIWPVDOQ 226
Db 153 VYLEKSKIRISFLIIGLAWLSALASPLAIFREYSLEIIPDFEIVACTERWPGSEK 212
QY 227 -LYKSYFLIFGIEFVGPVVTMTLCYARISRELWFKAVPGFQEQIRKRLCRKRTVLY 285
Db 213 SIYGTVYSSLLILVLPGLIISFYSYTRISWKLKSHVSPGAANDHYHQ--RQKTKM 269
QY 286 LMCILLAYVLCNAPFGFTIVRDFTPTVVKKHLYTAFYIVECIAMSNSINTLCFTV 345
Db 270 LVCVVYVAVSMLPLHAFQLAVDIDSHV-IDLKEYKLIFTVEHIIAMCSTFANPLLYGM 328
QY 346 KNDTVRYF 353
Db 329 NSNYKRAF 336

```

RESULT 11

```

US-08-513-974B-26
; Sequence 26, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; NUMBER OF INVENTIONS: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-513-974B-26

Query Match 18.0%; Score 370; DB 3; Length 370;
Best Local Similarity 28.5%; Pred. No. 6e-29;
Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;

QY 21 SVLNPHGATSPFENFSYSDYDMDPDEDEVTNSRTFFAAKIVGM--ALVGINLVCG- 77
Db 21 AVTTPANQSAEASAGNGSVAGADAPA-----VTPQSLQVLHQLKGLIVLLYVVVVVGL 75
QY 78 IGNFIFIAALVRYKKLNLIANLAIISDFLVAIVCCPFEMDYVYVYVYVYVYVYVYVYV 137
Db 76 VGNCLLVLIARVRLHNYTNFLIGNLALSDVLMCTACVPLTL-AYAFEPGRGWFGGLC 134
QY 138 TSVNYLRTVSLVSTNALLAIAIDRYLAIVHPRLPRMCKOTATGLIALVWTVSILAI 197
Db 135 HLVFFLQPVTVTVSVFTLTITIAVDRIYVVLVHPRLRRIRLSIRLSAYAVLAIALWALS 194

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QY 198 AVFTTETVLIVKSOEKIFCGQIWPVDQ---QIYKSYFLFIFGIEFVGPVVTMLCYAR 254
Db 195 A---VHTYHVELKPHDVRICEEFMGSGERQOLYANGLLL---VTYLLPLLVILLSYVR 247
QY 255 ISRELWFAVPGFQTEIRKRLRC-RRKTVLVLWCILTAYVLCWAPFYGFTIVRDFEFTV 313
Db 248 VSVKLRNRVPGCVTQSOADWDARRRTFCLLVVVVVFVAVCMPLPLHVNLLRLDLP-- 305
QY 314 FVKEKHYLT--AFYIVE--C--IAMSNSMINTLCFTVVKNDTVYFKKIMLLHW 361
Db 306 -----HAIDPYAFGLVOLLCHLWAMSSACYNPFYAWL-HDSFREELRKLVAW 353

RESULT 12

US-08-513-974B-323
; Sequence 323, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273

; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 323:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-513-974B-323

Query Match 18.0%; Score 370; DB 3; Length 370;
Best Local Similarity 28.5%; Pred. No. 6e-29;
Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;
QY 21 SVLNPHGAHATSPFFNFYSYSDYDMPLEDEDEVTNSRTFFFAKIVIGM--ALVGMILVCG- 77
Db 21 AVTTPANGSAEASAGNSVAGADAPA-----VTPFQSLQLVHQLKGLIVLLYSVVVVGL 75
QY 78 IGNEFTIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEMDYVVVRLSWEHGVL 137
Db 76 VGNCLLVLIARVRRLHNTVNFLLGNLALSVDLMCTACVPLTL-AYAFEPGRGWVFGGLC 134
QY 138 TSVNYLRTVSLVSTNALLAIDRYLAIVHPLRPMKQCTATGLIALVMTVSLIAIPS 197
Db 135 HLVTFLQPTVTVSVETLTIADVRYVYVHPLRRISRLSAYAVLAIWALSAVLALPA 194
QY 198 AFTTETVLIVKSOEKIFCGQIWPVDQ---QIYKSYFLFIFGIEFVGPVVTMLCYAR 254
Db 195 A---VHTYHVELKPHDVRICEEFMGSGERQOLYANGLLL---VTYLLPLLVILLSYVR 247
QY 255 ISRELWFAVPGFQTEIRKRLRC-RRKTVLVLWCILTAYVLCWAPFYGFTIVRDFEFTV 313
Db 248 VSVKLRNRVPGCVTQSOADWDARRRTFCLLVVVVVFVAVCMPLPLHVNLLRLDLP-- 305
QY 314 FVKEKHYLT--AFYIVE--C--IAMSNSMINTLCFTVVKNDTVYFKKIMLLHW 361
Db 306 -----HAIDPYAFGLVOLLCHLWAMSSACYNPFYAWL-HDSFREELRKLVAW 353

RESULT 13

US-09-172-353-5
; Sequence 5, Application US/09172353
; Patent No. 6197530
; GENERAL INFORMATION:
; APPLICANT: Stricker-Kongra, Alain
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
; FILE REFERENCE: 07334/102001
; CURRENT APPLICATION NUMBER: US/09/172,353
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-353-5

Query Match 18.0%; Score 370; DB 3; Length 370;
Best Local Similarity 28.5%; Pred. No. 6e-29;
Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;
QY 21 SVLNPHGAHATSPFFNFYSYSDYDMPLEDEDEVTNSRTFFFAKIVIGM--ALVGMILVCG- 77

| | | | |
|----|-----|---|-----|
| Db | 21 | AVTTTANQSAEASAGSNGSVAGADAPA-----VTFQSLQVLVHQLKGLVLVLLYVWVVUGL | 75 |
| QY | 78 | IGNFIIAALVRYKKLRNLTLNLANTLANISDLVAIVCCPEMDYVYVVRQLSWEGHVLIC | 137 |
| Db | 76 | VGNCLLVLIARVRLHNVTNFLIGNLALSVDLMCTACTAPLTL-AYAFEPGRWVFGGGLC | 134 |
| QY | 138 | TSVNYLRTVSLYVSTNALLATAIDEXLAIVHLEPRMKCQTATGLIALVTVTSILIAIDS | 197 |
| Db | 135 | HUVFELQPTVTVSVFTLTTIAVDRIYVVLVHPLRRISRLSAFVAVLAIWALSNAVLAFA | 194 |
| QY | 198 | AVFTTETVLVIYKSEKIFCGQINPVDQ---QLYKYSYFLFIEGIEFVGVPVMTTLCYAR | 254 |
| Db | 195 | A---VHTYHVELKPHDVRCLCEFGSQRORQIYAWGLL---VTYLLPLLVILLSYVR | 247 |
| QY | 255 | ISRELWFAKVPGFQEQIKRLRC-RRTVLVLMCLITAYVLWAPYGGTIVYRDFPTV | 313 |
| Db | 248 | VSVKLNRVVCVQTOSQNDWRARRRTFCLLVVVVFAVCLPULVFNILLRDLDP-- | 305 |
| QY | 314 | FVKEKHYLT--AFYIVE--C---IAMNSKNITLCFTVTKNDTVKYFKKIMLHW | 361 |
| Db | 306 | -----HAIDPYAGFLVOLICHLWLAWSACYNPFYIAML-HDSFREELRKLLVAM | 353 |

RESULT 14

```

US-08-776-971-21
: Sequence 21, Application US/08776971B
: Patent No. 6228984
: GENERAL INFORMATION:
: APPLICANT: Hinuma, Shuji
:             Habata, Yugo
:             Kawamata, Yuji
:             Hosoya, Masaki
:             Fujii, Ryo
:             Fukusumi, Shoji
:             Kitada, Chieko
: TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
: NUMBER OF SEQUENCES: 140
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
: STREET: 130 Water Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSEO for Windows Version 2.0
: CURRENT APPLICATION DATA: US/08/776,971B
: FILING DATE: 06-Feb-1997
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP96/03821
: FILING DATE: 28-DEC-1996
: APPLICATION NUMBER: JP 7/343371
: FILING DATE: 28-DEC-1995
: APPLICATION NUMBER: JP 8/59419
: FILING DATE: 15-MAR-1996
: APPLICATION NUMBER: JP 8/211805
: FILING DATE: 12-AUG-1996
: APPLICATION NUMBER: JP 8/246573
: FILING DATE: 18-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Conlin, David G.
: REGISTRATION NUMBER: 27,026
: REFERENCE/DOCKET NUMBER: 47176
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:

```

Search completed: October 7, 2003, 09:53:26
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 09:50:12 ; Search time 39 Seconds

(without alignments)
2600.376 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 HETMTGPMDDNAINSTSF.....LDLKTIGMPATEEVDICRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp-archaea:*

2: sp-bacteria:*

3: sp-fungi:*

4: sp-human:*

5: sp-invertebrate:*

6: sp-mammal:*

7: sp-mhc:*

8: sp-organelle:*

9: sp-phage:*

10: sp-plant:*

11: sp-rodent:*

12: sp-virus:*

13: sp-vertebrate:*

14: sp-unclassified:*

15: sp-rviro:*

16: sp-bacteriap:*

17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-----------|---------------------|
| 1 | 2055 | 100.0 | 393 | 4 Q8TCW9 | Q8TCW9 homo sapien |
| 2 | 2049 | 99.7 | 393 | 4 Q8NFJ7 | Q8NFJ7 homo sapien |
| 3 | 1915 | 93.2 | 393 | 6 Q8SPN2 | Q8SPN2 bos taurus |
| 4 | 1767 | 86.0 | 393 | 11 Q8R416 | Q8R416 rattus norv |
| 5 | 1766 | 85.9 | 384 | 4 Q8NFJ6 | Q8NFJ6 homo sapien |
| 6 | 1764 | 85.8 | 393 | 11 Q9JKL1 | Q9JKL1 mus musculus |
| 7 | 1719 | 83.6 | 384 | 6 Q8SPN1 | Q8SPN1 bos taurus |
| 8 | 1715.5 | 83.5 | 421 | 11 Q8R415 | Q8R415 rattus norv |
| 9 | 1703 | 82.9 | 355 | 4 Q9NTT0 | Q9NTT0 homo sapien |
| 10 | 1699.5 | 82.7 | 381 | 11 Q8K458 | Q8K458 mus musculus |
| 11 | 1020 | 49.6 | 220 | 11 Q8BIR4 | Q8BIR4 mus musculus |
| 12 | 407 | 19.8 | 449 | 5 Q9VB87 | Q9VB87 drosophila |
| 13 | 401.5 | 19.5 | 381 | 11 Q9BRC0 | Q9BRC0 rattus norv |
| 14 | 401 | 19.5 | 465 | 5 Q44426 | Q44426 lymanaea sta |
| 15 | 399.5 | 19.4 | 678 | 5 Q94736 | Q94736 stomoxys ca |
| 16 | 389.5 | 19.0 | 381 | 11 Q8BWL1 | Q8BWL1 mus musculus |

| | | | | | |
|----|-------|------|-----|-----------|---------------------|
| 17 | 382.5 | 18.6 | 519 | 5 Q9VAD2 | Q9VAD2 drosophila |
| 18 | 377.5 | 18.4 | 517 | 5 Q8TOS8 | Q8TOS8 drosophila |
| 19 | 367 | 17.9 | 504 | 5 Q9VX8 | Q9VX8 drosophila |
| 20 | 360.5 | 17.5 | 407 | 11 Q8BIR7 | Q8BIR7 mus musculus |
| 21 | 360 | 17.5 | 384 | 11 Q8BZV9 | Q8BZV9 mus musculus |
| 22 | 357.5 | 17.4 | 431 | 5 Q8TBD1 | Q8TBD1 urechis uni |
| 23 | 356 | 17.3 | 398 | 4 Q9UDE6 | Q9UDE6 homo sapien |
| 24 | 355.5 | 17.3 | 370 | 13 Q8UWL5 | Q8UWL5 fugu rubrip |
| 25 | 354.5 | 17.3 | 311 | 11 Q8RIR6 | Q8RIR6 cavia porce |
| 26 | 351 | 17.1 | 398 | 4 Q8NGQ8 | Q8NGQ8 homo sapien |
| 27 | 351 | 17.1 | 425 | 4 Q9HBV6 | Q9HBV6 homo sapien |
| 28 | 344 | 16.7 | 364 | 11 Q8BV78 | Q8BV78 mus musculus |
| 29 | 344 | 16.7 | 460 | 11 Q8BG12 | Q8BG12 mus musculus |
| 30 | 341 | 16.6 | 427 | 5 Q9N324 | Q9N324 caenorhabdi |
| 31 | 340.5 | 16.6 | 600 | 5 Q9VM75 | Q9VM75 drosophila |
| 32 | 339.5 | 16.5 | 367 | 13 Q9PVG0 | Q9PVG0 carassius a |
| 33 | 339 | 16.5 | 411 | 13 Q9M613 | Q9M613 gallus gall |
| 34 | 338 | 16.4 | 429 | 5 P92045 | P92045 lymanaea sta |
| 35 | 337.5 | 16.4 | 367 | 13 Q9PVF9 | Q9PVF9 carassius a |
| 36 | 337 | 16.4 | 380 | 13 Q9DQ66 | Q9DQ66 carassius a |
| 37 | 335 | 16.3 | 390 | 13 Q8JFP8 | Q8JFP8 bufo marinu |
| 38 | 333.5 | 16.2 | 377 | 13 Q8QCM3 | Q8QCM3 gallus gall |
| 39 | 332.5 | 16.2 | 402 | 5 Q964E5 | Q964E5 dugesia tig |
| 40 | 332.5 | 16.2 | 450 | 5 Q8T5J7 | Q8T5J7 anopheles g |
| 41 | 332 | 16.2 | 309 | 13 Q9D6J9 | Q9D6J9 bufo marinu |
| 42 | 329 | 16.0 | 385 | 11 Q8BQ97 | Q8BQ97 mus musculus |
| 43 | 327 | 15.9 | 452 | 11 Q9JKN0 | Q9JKN0 mus musculus |
| 44 | 326.5 | 15.9 | 346 | 6 Q9SKS6 | Q9SKS6 ovis aries |
| 45 | 323 | 15.7 | 422 | 11 Q8VHD7 | Q8VHD7 rattus norv |

ALIGNMENTS

RESULT 1

| ID | Q8TCW9 | PRELIMINARY; | PRT; | 393 AA. |
|----|---|--------------|------|---------|
| AC | Q8TCW9; | | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Created) | | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last sequence update) | | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last annotation update) | | | |
| DE | G protein-coupled receptor ZAQ (GPR73). | | | |
| GN | GPR73. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RA | Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.; | | | |
| RT | *Purification and identification of EG-VEGF family as cognate ligands for two orphan G protein-coupled receptors.*; | | | |
| RL | Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE-22314729; PubMed-12427552; | | | |
| RA | Soga T., Matsumoto S., Oda T., Saito T., Hiyama H., Takasaki J., | | | |
| RA | Kamohara M., Ohishi T., Matsushime H., Furuichi K.; | | | |
| RT | *Molecular cloning and characterization of prokineticin receptors.*; | | | |
| RL | Biochim. Biophys. Acta 1579:173-179(2002). | | | |
| DR | EMBL; AY089976; AAM1892.1; - | | | |
| DR | EMBL; AB084080; BAC24021.1; - | | | |
| DR | Interpro; IPR000276; GPCR_Rhodpsn. | | | |
| DR | Pfam; PF00001; 7tm_1; 1. | | | |
| DR | PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. | | | |
| DR | PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. | | | |
| KW | Receptor. | | | |
| SQ | SEQUENCE 393 AA; 44769 MW; OD36461CA99CAZC1 CRC64; | | | |

Query Match 100.0%; Score 2055; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.2e-183;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 METTMGFDDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60
DB 1 METTMGFDDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
DB 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
QY 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
QY 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
DB 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
RESULT 2
Q8NFJ7 PRELIMINARY; PRT; 393 AA.
AC Q8NFJ7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Prokineticin receptor 1.
GN PKRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22028034; PubMed=1186876;
RA Lin D.C.H., Bullock C.M., Ehler F.J., Chen J.L., Tian H., Zhou Q.Y.;
RT "Identification and Molecular Characterization of Two Closely Related
RT G Protein-coupled Receptors Activated by Prokineticins/Endocrine Gland
RT Vascular Endothelial Growth Factor.";
RL J. Biol. Chem. 277:19276-19280(2002).
DR EMBL; AF506287; AA48127.1; -.
DR Genbank; HGNC:4524; GPR73.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL2; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 44802 MW; AA085F33B789AEC7 CRC64;
Query Match 99.7%; Score 2049; DB 4; Length 393;
Best Local Similarity 99.5%; Pred. No. 4.2e-183;
Matches 391; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 METTMGFDDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60
DB 1 METTMGFDDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
DB 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
QY 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
QY 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
DB 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
RESULT 3
Q8SPN2 PRELIMINARY; PRT; 393 AA.
AC Q8SPN2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE G protein-coupled receptor 2A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;
RT "Purification and identification of EG-VGFP family as cognate ligands
RT for two orphan G protein-coupled receptors.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY089972; AA411888.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL2; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 44602 MW; CF302DD364D8A2CC CRC64;
Query Match 93.2%; Score 1915; DB 6; Length 393;
Best Local Similarity 92.4%; Pred. No. 1.4e-170;
Matches 363; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
QY 1 METTMGFDDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60
DB 1 METTMGFDDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
DB 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
QY 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
QY 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
DB 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
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DB 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
QY 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
QY 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
DB 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393
RESULT 3
Q8SPN2 PRELIMINARY; PRT; 393 AA.
AC Q8SPN2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE G protein-coupled receptor 2A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;
RT "Purification and identification of EG-VGFP family as cognate ligands
RT for two orphan G protein-coupled receptors.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY089972; AA411888.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL2; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 44602 MW; CF302DD364D8A2CC CRC64;
Query Match 93.2%; Score 1915; DB 6; Length 393;
Best Local Similarity 92.4%; Pred. No. 1.4e-170;
Matches 363; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
QY 1 METTMGFDDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60
DB 1 METTMGFDDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
DB 121 DYVVVRLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPKMCQTAT 180
QY 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
QY 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
DB 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLVCWAPF 300
QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLLH 360
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Db 301 YQFAIVRDFEFTVFYKKEHYLTAFTVVECIAMNSMINTVCFVTYKNTIKYFKKIMLLH 360
QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
Db 361 WKASNGKSSGDLDTKTGTGVPATEEVDICGLK 393
RESULT 4
Q8R416 PRELIMINARY: PRT: 393 AA.
AC Q8R416;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE G protein-coupled receptor ZAQ.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN: Sprague-Dawley;
RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;
RT "Purification and identification of EG-VGFR family as cognate ligands
for two orphan G protein-coupled receptors."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY089974; AAM11890.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 44507 MW; C75EC72B97E503A8 CRC64;
Query Match 86.0%; Score 1767; DB 11; Length 393;
Best Local Similarity 84.0%; Pred. No. 9.4e-157;
Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;
QY 1 MTTMGFDNDNATNSTSLVSLNPHGAHATSPFNFSYSDYDMPDLEDEDTNSRTFFA 60
Db 1 MTTVTGIGENTNTFTDFSSARDGSAETSLPTFSYGDYDMPDSEEDTNSRTFFA 60
QY 61 AKIVIGMALVGLMVCIGGNFIFIAALVRYKKRLNLTNLIANLAISDFLVAIVCCPFEM 120
Db 61 AKIVIGMALVGLMVCIGGNFIFIALARYKKRLNLTNLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVYRQLSWEHGHVLCISVNYLRTVSLVSTNALLAIDAIDRYLAIVHPLRPMKCQTAT 180
Db 121 DYVVYRQLSWEHGHVLCASVNYLRTVSLVSTNALLAIDAIDRYLAIVHPLRPMKCQTAA 180
QY 181 GLIALVMTYSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDOOLYKSYFLFIFGIE 240
Db 181 GLIFLWMSYILIAIPAAFTTETVLVIVSEKIFCGQIWPVDOQFYYSYFLVFLGLE 240
QY 241 FYGVPVMTLCARISRELWFAVPGFQTEQIRKRLCRKRVLVLMCLITAYVLCWAPF 300
Db 241 FYGVPVMTLCARVSRRELWFAVPGFQTEQIRKRLCRKRVLVGLCVLSAYVLCWAPF 300
QY 301 YGFTIVRDFEFTVFYKKEHYLTAFTVVECIAMNSMINTLCFVTYKNTIKYFKKIMLLH 360
Db 301 YGFTIVRDFEFTVFYKKEHYLTAFTVVECIAMNSMINTLCFVTYKNTIKYFKKIMLLH 360
QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
Db 361 WRASPSGSKASADLDLKTIGMPATEEVDICRLK 393
RESULT 5
Q8NFJ6 PRELIMINARY: PRT: 384 AA.
AC Q8NFJ6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
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DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Prokineticin receptor 2 (GPRG2).
GN PXR2 OR GPRG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22028034; PubMed=11886876;
RA Lin D.C.H., Bullock C.M., Ehler F.J., Chen J.L., Tian H., Zhou Q.Y.;
RT "Identification and Molecular Characterization of Two Closely Related
G Protein-coupled Receptors Activated by Prokineticins/Endocrine Gland
Vascular Endothelial Growth Factor."
RL J. Biol. Chem. 277:19276-19280(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=22314729; PubMed=12427552;
RA Soga T., Matsumoto S., Oda T., Saito T., Miyama H., Takasaki J.,
RA Kamohara M., Ohishi T., Matsushime H., Furuichi K.;
RT "Molecular cloning and characterization of prokineticin receptors."
RL Biochim. Biophys. Acta 1579:173-179(2002).
DR EMBL: AF506288; AAM48128.1; -.
DR EMBL: AB084081; BAC24022.1; -.
DR Genbank: HGNC:15836; GPR73L1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 384 AA; 43995 MW; 2D5BFA3655347B5E CRC64;
Query Match 85.9%; Score 1766; DB 4; Length 384;
Best Local Similarity 87.4%; Pred. No. 1.1e-156;
Matches 334; Conservative 20; Mismatches 28; Indels 0; Gaps 0;
QY 12 ATNTSTSLVSLNPHGAHATSPFNFSYSDYDMPDLEDEDTNSRTFFAIVIGMALVG 71
Db 3 AONGTSETPNFNPQDHASLSNFSYGDYDLPDDEDEDTKTFFAIVIGIALAG 62
QY 72 IMLVCGIGNFIFIAALVRYKKRLNLTNLIANLAISDFLVAIVCCPFEMDYVVYRQLSWE 131
Db 63 IMLVCGIGNFVIFIAALTRYKKRLNLTNLIANLAISDFLVAIICPPFEMDYVVYRQLSWE 122
QY 132 HGVLCSTVNYLRTVSLVSTNALLAIDAIDRYLAIVHPLRPMKCQTATGIALVMTVSI 191
Db 123 HGVLCASVNYLRTVSLVSTNALLAIDAIDRYLAIVHPLKPRMYQTASFIALVMTVSI 182
QY 192 LIAIPSAFTTETVLVIVKSEKIFCGQIWPVDOOLYKSYFLFIFGIEFYGVVMTLC 251
Db 183 LIAIPSAFTATETVLVIVKSEKIFCGQIWPVDOOLYKSYFLFIFGVEFYGVVMTLC 242
QY 252 YARISRELWFAVPGFQTEQIRKRLCRKRVLVLMCLITAYVLCWAPFYGFTIVRDFE 311
Db 243 YARISRELWFAVPGFQTEQIRKRLCRKRVLVLMCLITAYVLCWAPFYGFTIVRDFE 302
QY 312 TVFYKKEHYLTAFTVVECIAMNSMINTLCFVTYKNTIKYFKKIMLLHNSKASNGKSS 371
Db 303 TVFYKKEHYLTAFTVVECIAMNSMINTVCFVTYKNTIKYFKKIMLLHWPSPGSKSS 362
QY 372 ADLDLKTIGMPATEEVDICRLK 393
Db 363 ADLDLRTNGVPTTEVDICRLK 384
RESULT 6
Q9JKL1 PRELIMINARY: PRT: 393 AA.
ID Q9JKL1
AC Q9JKL1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
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DE G-protein coupled receptor GPR73 (Prokineticin receptor 1).
 GN GPR73 OR PKRI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20225484; PubMed=10760605;
 RA Parker R., Liu M., Eyre H.J., Copeland N.G., Gilbert D.J.,
 Crawford J., Sutherland G.R., Jenkins N.A., Herzog H.;
 RT "Y-receptor-like genes GPR72 and GPR73: molecular cloning, genomic
 organisation and assignment to human chromosome 11q21.1 and 2p14 and
 mouse chromosome 9 and 6.";
 RL Biochim. Biophys. Acta 1491:369-375(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22022134; PubMed=12024206;
 RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
 Weaver D.R., Leslie F.M., Zhou O.Y.;
 RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
 suprachiasmatic nucleus.";
 RL Nature 417:405-410(2002).
 DR EMBL: AF236082; AAF43706.1; -;
 DR MGD: AF487278; AAM49570.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1;
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1;
 DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1;
 KW Receptor.
 SQ SEQUENCE 393 AA: 44528 MW; 46F5E78C00DC871C CRC64;

Query Match 85.8%; Score 1764; DB 11; Length 393;
 Best Local Similarity 84.0%; Pred. No. 1.8e-156;
 Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 METTGFMDDNATNTSTFLSVLNPHGAHATSFPPNFYSYSDYDMPLEDEEDVTSRTFFA 60
 DB 1 METTVGALCENTDTFTDFFSALDQHEAQTSGLPFTFSYGDYDMPLEDEEDVTSRTFFA 60

QY 61 AKIVIGMALGVMLVCGIGNFTFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPEM 120
 DB 61 AKIVIGMALGVMLVCGIGNFTFIALARYKKLRNLTNLLIANLAISDFLVAIVCCPEM 120

QY 121 DYYVVRQLSWERGHVLCSTVNYLRTVSVLSTNALLAIAIDRYLAIVHPLPRMKCQTAT 180
 DB 121 DYYVVRQLSWERGHVLCASVNYLRTVSVLSTNALLAIAIDRYLAIVHPLPRMKCQTAA 180

QY 181 GLIALVWTVSILIAIPAAFTTETVLVIVROEKIFCGQIWPVDQOYFYSYELLVFGLE 240
 DB 181 GLIFLWMSVSIILIAIPAAFTTETVLVIVROEKIFCGQIWPVDQOYFYSYELLVFGLE 240

QY 241 FVGPPVMTLCYARISRELWFKAVPGFQEQIRKRLCRKRTVLVLMCLITAYVLCNAPF 300
 DB 241 FVGPPVMTLCYARISRELWFKAVPGFQEQIRKRLCRKRTVLVLMCLITAYVLCNAPF 300

QY 301 YGTTIVRDFPPTVVKKEHYLTAIFYVECIAMNSMINTLCFTVVKNDTVYFKKIMLLH 360
 DB 301 YGTTIVRDFPPTVVKKEHYLTAIFYVECIAMNSMINTLCFTVVKNDTVYFKKIMLLH 360

QY 361 WKASNYGKSSADLDKTIKMPATEEVDICRLK 393
 DB 361 WRASPSGSKASADLDKTIKMPATEEVDICRLK 393

RESULT 7
 Q8SPN1 PRELIMINARY; PRT; 384 AA.
 AC Q8SPN1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE G protein-coupled receptor 15E.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;
 RT "Purification and identification of EG-VSGF family as cognate ligands
 for two orphan G protein-coupled receptors.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AV089973; AAM11889.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1;
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1;
 DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1;
 KW Receptor.
 SQ SEQUENCE 384 AA: 44138 MW; 997895960EEB2DD4 CRC64;

Query Match 83.6%; Score 1719; DB 6; Length 384;
 Best Local Similarity 84.3%; Pred. No. 2.8e-152;
 Matches 322; Conservative 29; Mismatches 31; Indels 0; Gaps 0;

QY 12 ATNTSTFLSVLNPHGAHATSFPPNFYSYSDYDMPLEDEEDVTSRTFFAIVIGMALVG 71
 DB 3 AQGNASFPANFSIPOEHASSLPENFSDYDMPLEDEEDMTKTQTFPAKIVIGVALVG 62

QY 72 IMLVCGIGNFTFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPEMDYVYVRLSWE 131
 DB 63 IMLTGCIGNFTFIALTRYKKLRNLTNLLIANLAISDFLVAIVCCPEMDYVYVHQLSWE 122

QY 132 HGVLCSTVNYLRTVSVLSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIALVWTVSI 191
 DB 123 HGVLCACINYLRTVSVLSTNALLAIAIDRYLAIVHPLPRMNYQTASFIALVWTVSI 182

QY 192 LIAIPSAVYTTETVLVIVKSEKIFCGQIWPVDQOYLYKSYFLFIFGIEFVGPPVMTLC 251
 DB 183 LISIPSAVYTKETVLVIVKSKIFCGQVMPVDQOYLYKSYFLFVFGIEFVGPPVMTLC 242

QY 252 YARISRELWFKAVPGFQEQIRKRLCRKRTVLVLMCLITAYVLCNAPFYGTTIVRDFP 311
 DB 243 YARISRELWFKAVPGFQEQIRKRLCRKRTVLVLMCLITAYVLCNAPFYGTTIVRDFP 302

QY 312 TVFVKEKHYLTAIFYVECIAMNSMINTLCFTVVKNDTVYFKKIMLLHWKASNYGKSS 371
 DB 303 TVFVKEKHYLTAIFYVECIAMNSMINTVCFVTVKNSTMKYFKKIMLLHWKASNYGKSS 362

QY 372 ADLDKTIKMPATEEVDICRLK 393
 DB 363 ADLDKTSRLPATEEVDICRLK 384

RESULT 8
 Q8R415 PRELIMINARY; PRT; 421 AA.
 AC Q8R415;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE G protein-coupled receptor 15E.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;
 RT "Purification and identification of EG-VSGF family as cognate ligands
 for two orphan G protein-coupled receptors.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY089975; AAM11891.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEPT_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 421 AA; 47870 MW; AC98D113DICG4DC3 CRC64;

Query Match 83.5%; Score 1715.5; DB 11; Length 421;
 Best Local Similarity 85.3%; Pred. No. 6.6e-152;
 Matches 324; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY 14 NSTSFLSLNPHGAHATSEFPNFSYSDYDPLDEDEDTNSRTFFAAKIVIGMALVGM 73
 DB 43 NGNTSFADLPNPQDQVSLPLNYSYGYDIPLDDEDDVTKTQFFAAKIVIGMALGIM 102
 QY 74 LVCGIGNFIFIAALVRYKKRLNLTLLIANLAISDFLVAIVCCPFEMDYVYVROLSEHG 133
 DB 103 LVCGVGNFVFAALARYKKRLNLTLLIANLAISDFLVAIVCCPFEMDYVYVROLSEHG 162
 QY 134 HVLCISVNYLRTVSLVSTNALLATAIDRYLAIVHPLPRMKCQTATGLIALVTVSILI 193
 DB 163 HVLCASVNYLRTVSLVSTNALLATAIDRYLAIVHPLK-RMNYQTASFLLALVWVSYILI 221
 QY 194 AIPSAFTTETVLVIVKSOEKIFCGIWPVDQQLYKSYFLFIFGIEFVGPVWTMLCYA 253
 DB 222 AIPSAFTTETVLVIVKQKRLFCQIWPVDQQLYKSYFLFVGLFVGPVWTMLCYA 281
 QY 254 RISRELMFKAVPGFQTEQIRKRLCRRRTVLMCILTAIVLCWAPFYGFTIVRDFFTV 313
 DB 282 RISQELMFKAVPGFQTEQIRKRLCRRRTVLMCILTAIVLCWAPFYGFTIVRDFFTL 341
 QY 314 FYKEKHLYTAFVIVCIAMNSMINTLCFTVTKNDTVKFKIMLLHWKASVNGKSSAD 373
 DB 342 VYKEKHLYTAFVIVCIAMNSMINTLCFTVTKNTHYFKKMLLHWKASVNGKSSAD 401
 QY 374 LDLKTIGMPATEEVDICIRLK 393
 DB 402 LDLKTSGVPATEEVDICIRLK 421

RESULT 9

Q9NTT0
 ID Q9NTT0 PRELIMINARY; PRT; 355 AA.
 AC Q9NTT0;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE DJ680N4.3 (Novel G-protein coupled receptor similar to mouse GPR73) (Fragment).
 DE DJ680N4.3.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Collier R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL121755; CAB89854.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEPT_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 SQ SEQUENCE 355 AA; 40884 MW; 63F308D775B5B3A6 CRC64;

Query Match 82.9%; Score 1703; DB 4; Length 355;
 Best Local Similarity 90.1%; Pred. No. 8e-151;
 Matches 320; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 39 YSDYDMPLEDEDEDTNSRTFFAAKIVIGMALVGMVCGIGNFIFIAALVRYKKRLNLTN 98
 DB 1 YGYDYLPMDEDEDDMTKTRTFFAAKIVIGIALAGIMLVCGIGNFVFTAAALTRYKKRLNLTN 60
 QY 99 LLIANLAISDFLVAIVCCPFEMDYVYVROLSEHGVLCTSVNYLRTVSLVSTNALLAI 158
 DB 61 LLIANLAISDFLVAIVCCPFEMDYVYVROLSEHGVLCTSVNYLRTVSLVSTNALLAI 120
 QY 159 AIDRYLAIVHPLPRMKCQTATGLIALVTVSILIIPSAYFTTETVLVIVKSOEKIFCG 218
 DB 121 AIDRYLAIVHPLPRMNYQTASFLLALVWVSYILIIPSAYFATETVFLTVKSOEKIFCG 180
 QY 219 QIWPVDQQLYKSYFLFIFGIEFVGPVWTMLCYARISRELMFKAVPGFQTEQIRKRLC 278
 DB 181 QIWPVDQQLYKSYFLFIFGIEFVGPVWTMLCYARISRELMFKAVPGFQTEQIRKRLC 240
 QY 279 RRTKTVLMCILTAIVLCWAPFYGFTIVRDFFTVFKKHLYTAFVIVCIAMNSMIN 338
 DB 241 RRTKTVLMCILTAIVLCWAPFYGFTIVRDFFTVFKKHLYTAFVIVCIAMNSMIN 300
 QY 339 TLFCTVTKNDTVKFKIMLLHWKASVNGKSSADLDLKTIGMPATEEVDICIRLK 393
 DB 301 TVCFVTYKNTTHYFKKMLLHWKASVNGKSSADLDLRTNGVPTTEEVDICIRLK 355

RESULT 10

Q8K458
 ID Q8K458 PRELIMINARY; PRT; 381 AA.
 AC Q8K458;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Prokineticin receptor 2 (DJ680N4.3).
 GN GPR73L1 OR PRK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22022134; PubMed=12024206;
 RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
 RA Weaver D.R., Leslie F.M., Zhou Q.Y.;
 RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
 RT suprachiasmatic nucleus";
 RL Nature 417:405-410(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata, and Thymus;
 RX MEDLINE=22354583; PubMed=12466851;
 RA The FANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 DR EMBL: AF487279; AAM49571.1; -
 DR EMBL: AK041586; BAC30994.1; -
 DR EMBL: AK080980; BAC38103.1; -
 DR MGD: MGI:2181363; Gpr73l1.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEPT_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 381 AA; 43375 MW; 1981FD101324166D CRC64;

Query Match 82.7%; Score 1699.5; DB 11; Length 381;
 Best Local Similarity 85.0%; Pred. No. 1.8e-150;
 Matches 323; Conservative 26; Mismatches 28; Indels 3; Gaps 1;

Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]
RN SEQUENCE FROM N.A.
RP STRAIN-Wistar; TISSUE-Small intestine;
RC Voisin T., Gouman M., LaBurthe M.;
RT "Cloning of a cDNA encoding a rat type 2 neuro-peptide Y/peptide YY
receptor expressed in intestinal epithelial crypt cells."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AY004257; AAF89094.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; 1.
KW Receptor.
SQ SEQUENCE 381 AA; 42510 MW; 659327904B288BC7 CRC64;

Query Match 19.5%; Score 401.5; DB 11; Length 381;
Best Local Similarity 28.6%; Pred. No. 3.4e-29;
Matches 98; Conservative 83; Mismatches 147; Indels 15; Gaps 6;

QY 43 DMPLEDEVDVNSRTFFAAKIVIGMALVIGIMLVCGIGNFIFIAALVRYKKLRNLNLLIA 102
DB 31 ELPPDPELIDSTKLVEVQVLLIAYCSIIILGVVGNLSLVHVVVKFSMTVTNFFIA 90
QY 103 NLAISDFLVAIVCCPEMDYVVRQLSWEHGVLTCTSVNVLRTSVLSYSTNALLAIDR 162
DB 91 NLAVADLVNTLCLEPTLTITLWGE--WKMGVPLCHLVPAOGLAVQVSTITLTVALDR 148
QY 163 YLAIVHPLPRMKCQTATGLIALVMTVSILAIIPSAFYTTETVLVIVKSEIFCGQIWP 222
DB 149 HRCIVVHLESKISKISFLIIGLVGVSALLAPLAIFREYSILRIIPDFEIVACTEKWP 208
QY 223 VQOOLYKS-YELFIFGIEFVGVTMTLCYARISRELWFKAVPGFQFQIKRRLCRKK 281
DB 209 GEKSVYGTVYSLTLLIYLVPLGIISFSYTRWSKLNKHYSPGAASDHYHQ---RHK 265
QY 282 TVLVLMCIATAVLVCAVPGYFTIVRDFPTVFKKHYLTAFYVECIANSNMINTLC 341
DB 266 TTKMLVCVVVFAVSWLPPLHAFQLAVIDSHV-LDLKEYKLIFTVPHIIMCSTFANPLL 324
QY 342 FTVYKNDYKVF-----KKIMLLHWKASYNGKSSADLDLK 377
DB 325 YGMNSNRYKAFISAPRCQRLDAIHSEVSMY-FRAKKNLVYK 366

RESULT 14
O44426

ID O44426 PRELIMINARY; PRT; 465 AA.
AC O44426;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cardioexcitatory receptor.
GN GR106.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=5523;

[1]
RN SEQUENCE FROM N.A.
RX MEDLINE-99042058; PubMed-9822740;
RA Tensen C.P., Cox K.J., Smit A.B., van der Schors R.C., Meyerhof W.,
RA Richter D., Planta R.J., Hermann P.M., van Minnen J., Geraerts W.P.,
RA Knol J.C., Burke J.F., Vreugdenhil E., van Heerikhuizen H.;
RT "The lymnaea cardioexcitatory peptide (LYCEP) receptor: a G-protein-
coupled receptor for a novel member of the RFamide neuro-peptide
family."
RL J. Neurosci. 18:9812-9821(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF037444; AAB92258.1; -.

Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]
RN SEQUENCE FROM N.A.
RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaninker J.S., Prochman S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Carlson J.W., Celniker S.E.,
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak P., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[4]
RN SEQUENCE FROM N.A.
RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[5]
RN SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

EMBL: AE003759; AAF56655.2;
DR FlyBase; FBgn0004842; NephY.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
SQ SEQUENCE 449 AA; 51869 MW; FD8DOB3D70476EC1 CRC64;

Query Match 19.8%; Score 407; DB 5; Length 449;
Best Local Similarity 30.0%; Pred. No. 1.3e-29;
Matches 115; Conservative 70; Mismatches 128; Indels 70; Gaps 15;

QY 9 DDNAIN---TSTFSLVNLPHGAAHATSPFNFSYSDYDMPLEDEVDVNSRTFFAAKIVI 65
DB 41 DDEGSNYGCGTITLSLQFETYNIVM-KNFSCDDYDL---LSEDMWSSAYF---KIIV 93
QY 66 GMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCP-----FE 119
DB 94 YMLYIPFIFALINGVGVYVSTPMTVTNYFIASLAIGDILASFFCVPSFISLEFI 153
QY 120 MDYVVVQLSWEHGVLTCTSVNVLRTSVLSYSTNALLAIDRYLAIVHPLPRMKCOTA 179
DB 154 LNY-----WPLGLAHCFFVNSQAVSVLSVAYTLVAISIDRYALMPLKPRITRYA 206
QY 180 TGLIALVMTVSILAIIP-----SAFYTTETVLVIVKSEIFCGQIWPVQOOLY 228
DB 207 TFIAGVWEIATATALPIPIVSGLDIPMSPHWT-----KCEKYICREMPSPRTQY 257
QY 229 KSYFLFIFGIEFVGVTMTLCYARISRELWFKAVPG-FQEQIRKRLCRKTVLVLM 287
DB 258 Y-YTSLFALQFVPLGVLFYFARITIRVAKRPFGEAETNRDQWAKSKRMVQMDL 315
QY 288 CILTAVLVCAVPGYFTIVR-----FFPTVFKKHYLTAFYVECIANSNMINTL- 340
DB 316 TVTVVFTCCWLPFNILQLLNLNDEFAHWDPYV-----WEAFHWLANSCHCCYNPII 367
QY 341 CFVTVKNDYKVKFK--IMLLH 360
DB 368 YCYNNAR-----FRSGFVQLMH 384

RESULT 13

Q9ERCO
ID Q9ERCO PRELIMINARY; PRT; 381 AA.
AC Q9ERCO;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Neuro-peptide Y/peptide YY-2 receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

Search completed: October 7, 2003, 09:53:01
Job time : 43 secs